

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

UTILITY APPLICATION AND FEE TRANSMITTAL (1.53(b))

ASSISTANT COMMISSIONER FOR PATENTS
Box Patent Application
Washington, D.C. 20231

Sir:

Transmitted herewith for filing is the patent application of

First named Inventor

or Application Identifier: Jens Bukh, 5805 Sonoma Road, Maryland 20817
Roger H. Miller, 15504 White Willow Lane, Rockville, Maryland 20853
Robert H. Purcell, 17517 White Grounds Road, Boyds, Maryland 20841

For: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE I AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS
DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

Enclosed are:

[X] 253 page(s) of specification, including 162 pages of Sequence Listing, 1 page(s) of Abstract,
10 page(s) of claims

[X] 89 sheets of drawing [] formal [X] informal

[X] 2 page(s) of Declaration and Power of Attorney

[] Unsigned

[] Newly Executed

[X] Copy from prior application

[] Deletion of inventors including Signed Statement under 37 C.F.R. § 1.63(d)(2)

[X] Incorporation by Reference: The entire disclosure of the prior application, from which a copy of the combined declaration and power of attorney is supplied herein, is considered as being part of the disclosure of the accompanying application and is incorporated herein by reference.

[] Microfiche Computer Program (Appendix)

[X] 162 page(s) of Sequence Listing

[X] computer readable disk containing Sequence Listing

[X] Statement under 37 C.F.R. § 1.821(f) that computer and paper copies of the Sequence Listing are the same

[] Certified copy of Priority Document(s)

[] English translation documents

- ☒ Information Disclosure Statement
- ☐ Copy of cited references
- ☐ Preliminary Amendment
- ☒ Return receipt postcard (MPEP 503)
- ☒ Assignment Papers (assignment cover sheet and assignment documents)
- ☐ A check in the amount of \$40.00 for recording the Assignment.
- ☒ Assignment papers filed in parent application Serial No. 08/290,665.
- ☐ Certification of chain of title pursuant to 37 C.F.R. § 3.73(b).
- ☒ This is a ☐ continuation ☒ divisional ☐ continuation-in-part (C-I-P) of prior application serial no. 08/290,665.
- ☒ Cancel in this application original claims 21-31 of the parent application before calculating the filing fee. (At least one original independent claim must be retained for filing purposes.)
- ☐ A Preliminary Amendment is enclosed. (Claims added by this Amendment have been properly numbered consecutively beginning with the number following the highest numbered original claim in the prior application.
- ☒ The status of the parent application is as follows:
- ☐ A Petition For Extension of Time and a Fee therefor has been or is being filed in the parent application to extend the term for action in the parent application until .
- ☐ A copy of the Petition for Extension of Time in the co-pending parent application is attached.
- ☒ No Petition For Extension of Time and Fee therefor are necessary in the co-pending parent application.
- ☐ Please abandon the parent application at a time while the parent application is pending or at a time when the petition for extension of time in that application is granted and while this application is pending has been granted a filing date, so as to make this application co-pending.
- ☐ Transfer the drawing(s) from the parent application to this application.
- ☒ Amend the specification by inserting before the first line the sentence:
This is a ☐ continuation ☒ divisional ☐ continuation-in-part of co-pending application Serial No. 08/290,665 filed August 15, 1994; which is a continuation-in-part of application Serial No. 08/086,428 filed on June 29, 1993, now U.S. Patent No. 5,514,539.

I. CALCULATION OF APPLICATION FEE						Basic Fee
	Number Filed		Number Extra	Rate	\$ 790.00	
Total						
Claims	55	-20 =	35	x	\$22.00	\$ 770.00
Independent						
Claims	18	- 3 =	15	x	\$82.00	\$1230.00
Multiple Dependent Claims						
	[X] yes		Additional fee	=	\$270.00	\$ 270.00
	[] no		Additional fee	=	NONE	
						Total: \$3060.00

- [] A statement claiming small entity status is attached or has been filed in the above-identified parent application and its benefit under 37 C.F.R. § 1.28(a) is hereby claimed. Reduced fees under 37 C.F.R. § 1.9(F) (50% of total) paid herewith \$_____.
- [X] A check in the amount of \$_____ in payment of the application filing fees is attached.
- [] Charge Fee(s) to Deposit Account No. 13-4500. Order No._____. A DUPLICATE COPY OF THIS SHEET IS ATTACHED.
- [X] The Assistant Commissioner is hereby authorized to charge any additional fees which may be required for filing this application, or credit any overpayment to Deposit Account No. 13-4500 Order No. 2026-4116US2. A DUPLICATE COPY OF THIS SHEET IS ATTACHED.

Respectfully submitted,

MORGAN & FINNEGAN, L.L.P.

Dated: May 26, 1998

By:

Richard W. Bork
Richard W. Bork
Registration No. 36,459

CORRESPONDENCE ADDRESS:

Morgan & Finnegan L.L.P.
345 Park Avenue
New York, New York 10154
(212) 758-4800
(212) 751-6849 Facsimile

FORM: UTL-TRAN.NY
Rev. 1/16/98

Applicant(s) :	Bukh, et al.	Group Art Unit :	To Be Assigned
Serial No. :	To Be Assigned	Examiner :	To Be Assigned
Filed :	May 26, 1998		
For :	NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES		

TRANSMITTAL REMARKS

Sir:

This paper is submitted to inform the Examiner of certain minor changes that have been made to the copy of the specification of parent application number 08/290,665 submitted herewith.

In particular, the claim to priority on page 1 of the application and the prior and current application data in the Sequence Listing have been updated. In addition, the number "585" at the end of the last line of SEQ ID NO:154 in the Sequence Listing has been changed to "573".

These changes are believed to be ministerial in nature and do not therefore result in the introduction of new matter into the specification.

The Commissioner is hereby authorize to charge any fees which may be required for this paper or credit any overpayment to deposit account number 13-4500, order number 2026-4116US2. A DUPLICATE OF THIS SHEET IS ATTACHED.

Early and favorable action by the Examiner is earnestly solicited.

Respectfully submitted,

MORGAN & FINNEGAN, L.L.P.

Dated: May 26, 1998

By: Richard W. Bork
Richard W. Bork
Registration No. 36,459

Mailing Address:

MORGAN & FINNEGAN, L.L.P.
345 Park Avenue
New York, New York 10154
(212) 758-4800
(212) 751-6849 Telecopier

Applicant(s) :	Bukh, et al.	Group Art Unit :	To Be Assigned
Serial No. :	To Be Assigned	Examiner :	To Be Assigned
Filed :	May 26, 1998		
For :	NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES		

Sir:

I hereby certify that:

[X] The paper Sequence Listing and computer readable Sequence Listing submitted herewith are identical (37. C.F.R. §1.821(f)).

[] The substitute paper Sequence Listing and substitute computer readable Sequence Listing submitted herewith are identical. No new matter is included (37 C.F.R. §1.825(b)).

Respectfully submitted,

MORGAN & FINNEGAN, L.L.P.

Dated: May 26, 1998

By: Richard W. Bork
Richard W. Bork
Registration No. 36,459

Mailing Address:

MORGAN & FINNEGAN, L.L.P.
345 Park Avenue
New York, New York 10154
(212) 758-4800
(212) 751-6849 Telecopier

Title of the Invention

NUCLEOTIDE AND DEDUCED AMINO ACID
SEQUENCES OF THE ENVELOPE 1 AND CORE
GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM
THESE SEQUENCES IN DIAGNOSTIC METHODS
AND VACCINES

The present application is a divisional
application of pending U.S. Application Serial No.
08/290,665, filed August 15, 1994, which is a continuation-
in-part of U.S. Application Serial No. 08/086,428, filed on
June 29, 1993, now U.S. Patent No. 5,514,539.

Field Of Invention

The present invention is in the field of
hepatitis virology. The invention relates to the complete
nucleotide and deduced amino acid sequences of the envelope
1 (E1) and core genes of hepatitis C virus (HCV) isolates
from around the world and the grouping of these isolates
into fourteen distinct HCV genotypes. More specifically,
this invention relates to oligonucleotides, peptides and
recombinant proteins derived from the envelope 1 and core
gene sequences of these isolates of hepatitis C virus and
to diagnostic methods and vaccines which employ these
reagents.

Background Of Invention

Hepatitis C, originally called non-A, non-B
hepatitis, was first described in 1975 as a disease
serologically distinct from hepatitis A and hepatitis B
(Feinstone, S.M. et al. (1975) N. Engl. J. Med. 292:767-
770). Although hepatitis C was (and is) the leading type
of transfusion-associated hepatitis as well as an important
part of community-acquired hepatitis, little progress was
made in understanding the disease until the recent
identification of hepatitis C virus (HCV) as the causative
agent of hepatitis C via the cloning and sequencing of the

° HCV genome (Choo, A.L. et al. (1989) Science 288:359-362).
The sequence information generated by this study resulted
in the characterization of HCV as a small, enveloped,
positive-stranded RNA virus and led to the demonstration
that HCV is a major cause of both acute and chronic
5 hepatitis worldwide (Weiner, A.J. et al. (1990) Lancet
335:1-3). These observations, combined with studies
showing that over 50% of acute cases of hepatitis C
progress to chronicity with 20% of these resulting in
cirrhosis and an undetermined proportion progressing to
10 liver cancer, have led to tremendous efforts by
investigators within the hepatitis C field to develop
diagnostic assays and vaccines which can detect and prevent
hepatitis C infection.

The cloning and sequencing of the HCV genome by
15 Choo et al. (1989) has permitted the development of
serologic tests which can detect HCV or antibody to HCV
(Kuo, G. et al. (1989) Science 244:362-364). In addition,
the work of Choo et al. has also allowed the development of
methods for detecting HCV infection via amplification of
20 HCV RNA sequences by reverse transcription and cDNA
polymerase chain reaction (RT-PCR) using primers derived
from the HCV genomic sequence (Weiner, A.J. et al.).
However, although the development of these diagnostic
methods has resulted in improved diagnosis of HCV
25 infection, only approximately 60% of cases of hepatitis C
are associated with a factor identified as contributing to
transmission of HCV (Alter, M.J. et al. (1989) JAMA
262:1201-1205). This observation suggests that effective
control of hepatitis C transmission is likely to occur only
30 via universal pediatric vaccination as has been initiated
recently for hepatitis B virus. Unfortunately, attempts to
date to protect chimpanzees from hepatitis C infection via
administration of recombinant vaccines have had only
limited success. Moreover, the apparent genetic
35 heterogeneity of HCV, as indicated by the recent assignment

° of all available HCV isolates to one of four genotypes, I-IV (Okamoto, H. et al. (1992) J. Gen. Virol; 73:673-679), presents additional hurdles which must be overcome in order to develop accurate and effective diagnostic assays and vaccines.

5 For example, one possible obstacle to the development of effective hepatitis C vaccines would arise if the observed genetic heterogeneity of HCV reflects serologic heterogeneity. In such a case, the most genetically diverse strains of HCV may then represent
10 different serotypes of HCV with the result being that infection with one strain may not protect against infection with another. Indeed, the inability of one strain to protect against infection with another strain was recently noted by both Farci et al. (Farci, P. et al. (1992) Science
15 258:135-140) and Prince et al. (Prince, A.M. et al. (1992) J. Infect. Dis. 165:438-443), each of whom presented evidence that while infection with one strain of HCV does modify the degree of the hepatitis C associated with the reinfection, it does not protect against reinfection with a
20 closely related strain. The genetic heterogeneity among different HCV strains also increases the difficulty encountered in developing RT-PCR assays to detect HCV infection since such heterogeneity often results in false-negative results because of primer and template mismatch. In addition, currently used serologic tests for detection
25 of HCV or for detection of antibody to HCV are not sufficiently well developed to detect all of the HCV genotypes which might exist in a given blood sample. Finally, in terms of choosing the proper treatment modality
30 to combat hepatitis infection, the inability of presently available serologic assays to distinguish among the various genotypes of HCV represents a significant shortcoming in that recent reports suggest that an HCV-infected patient's response to therapy might be related to the genotype of the
35 infectious virus (Yoshioka, K. et al. (1992) Hepatology

16:293-299; Kanai, K. et al. (1992) Lancet 339:1543; Lan,
J.Y.N. et al. (1992) Hepatology 16:209A). Indeed, the data
presented in the above studies suggest that the closely
related genotypes I and II are less responsive to
interferon therapy than are the closely related genotypes
5 III and IV. Moreover, preliminary data by Pozzato et al.
(Pozzato, G. et al. (1991) Lancet 338:509) suggests that
different genotypes may be associated with different types
or degrees of clinical disease. Taken together, these
studies suggest that before effective vaccines against HCV
10 infection can be developed, and indeed, before more
accurate and effective methods for diagnosis and treatment
of HCV infection can be produced, one must obtain a greater
knowledge about the genetic and serologic diversity of HCV
isolates.

15 In a recent attempt to gain an understanding of
the extent of genetic heterogeneity among HCV strains, Bukh
et al. carried out a detailed analysis of HCV isolates via
the use of PCR technology to amplify different regions of
the HCV genome (Bukh, J. et al. (1992a) Proc. Natl. Acad.
20 Sci. 89:187-191). Following PCR amplification, the 5'-
noncoding (5' NC) portion of the genomes of various HCV
isolates were sequenced and it was found that primer pairs
designed from conserved regions of the 5' NC region of the
HCV genome were more sensitive for detecting the presence
25 of HCV than were primer pairs representing other portions
of the genome (Bukh, J. et al. (1992b) Proc. Natl. Acad.
Sci. U.S.A. 89:4942-4946). In addition, the authors noted
that although many of the HCV isolates examined could be
classified into the four genotypes described by Okamoto et
30 al. (1992), other previously undescribed genotypes emerged
based on genetic heterogeneity observed in the 5' NC region
of the various isolates. One of the most prominent of
these newly noted genotypes comprised a group of related
viruses that contained the most genetically divergent 5' NC
35 regions of those studied. This group of viruses,

- ° tentatively classified as a fifth genotype, are very similar to strains recently described by others (Cha, T.-A et al. (1992) Proc. Natl. Acad. Sci. U.S.A. 89:7144-7148; Chan, S-W. et al. (1992) J. Gen. Virol., 73:1131-1141 and Lee, C-H et al. (1992) J. Clin. Microbio. 30:1602-1604).
- 5 In addition, at least four more putative genotypes were identified thereby providing evidence that the genetic heterogeneity of HCV was more extensive than previously appreciated.

However, while the studies of Bukh et al. (1992a and b) provided new and useful information on the genetic heterogeneity of HCV, it is widely appreciated by those skilled in the art that the three structural genes of HCV, core (C), envelope (E1) and envelope 2/nonstructural 1 (E2/NS1) are the most important for the development of serologic diagnostics and vaccines since it is the product of these genes that constitutes the hepatitis C virion. Thus, a determination of the nucleotide sequence of one or all of the structural genes of a variety of HCV isolates would be useful in designing reagents for use in diagnostic assays and vaccines since a demonstration of genetic heterogeneity in a structural gene(s) of HCV isolates might suggest that some of the HCV genotypes represent distinct serotypes of HCV based upon the previously observed relationship between genetic heterogeneity and serologic heterogeneity among another group of single-stranded, positive-sense RNA viruses, the picornaviruses (Ruechert, R.R. "Picornaviridae and their replication", in Fields, B.N. et al., eds. Virology, New York: Raven Press, Ltd. (1990) 507-548).

10
15
20
25

30

Summary of Invention

The present invention relates to cDNAs encoding the complete nucleotide sequence of either the envelope 1 (E1) gene or the core (C) gene of an isolate of human hepatitis C virus (HCV).

35

° The present invention also relates to the nucleic acid and deduced amino acid sequences of these E1 and core cDNAs.

It is an object of this invention to provide synthetic nucleic acid sequences capable of directing
5 production of recombinant E1 and core proteins, as well as equivalent natural nucleic acid sequences. Such natural nucleic acid sequences may be isolated from a cDNA or genomic library from which the gene capable of directing synthesis of the E1 or core proteins may be identified and
10 isolated. For purposes of this application, nucleic acid sequence refers to RNA, DNA, cDNA or any synthetic variant thereof which encodes for peptides.

The invention also relates to the method of preparing recombinant E1 and core proteins derived from E1
15 and core cDNA sequences respectively by cloning the nucleic acid encoding either the recombinant E1 or core protein and inserting the cDNA into an expression vector and expressing the recombinant protein in a host cell.

The invention also relates to isolated and
20 substantially purified recombinant E1 and core proteins and analogs thereof encoded by E1 and core cDNAs respectively.

The invention further relates to the use of recombinant E1 and core proteins, either alone, or in combination with each other, as diagnostic agents and as
25 vaccines.

The present invention also relates to the recombinant production of the core protein of the present invention to contain a second protein on its surface and therefore serve as a carrier in a multivalent vaccine
30 preparation. Further, the present invention relates to the use of the self aggregating core or envelope proteins as a drug delivery system for anti-virals.

The invention also relates to the use of single-stranded antisense poly- or oligonucleotides derived from
35 E1 or core cDNAs, or from both E1 and core cDNAs, to

- ° inhibit expression of hepatitis C E1 and/or core genes.

The invention further relates to multiple computer-generated alignments of the nucleotide and deduced amino acid sequences of the E1 and core cDNAs. These multiple sequence alignments produce consensus sequences which serve to highlight regions of homology and non-homology between sequences found within the same genotype or in different genotypes and hence, these alignments can be used by one skilled in the art to design peptides and oligonucleotides useful as reagents in diagnostic assays and vaccines.

The invention therefore also relates to purified and isolated peptides and analogs thereof derived from E1 and core cDNA sequences.

The invention further relates to the use of these peptides as diagnostic agents and vaccines.

The present invention also encompasses methods of detecting antibodies specific for hepatitis C virus in biological samples. The methods of detecting HCV or antibodies to HCV disclosed in the present invention are useful for diagnosis of infection and disease caused by HCV and for monitoring the progression of such disease. Such methods are also useful for monitoring the efficacy of therapeutic agents during the course of treatment of HCV infection and disease in a mammal.

The invention also provides a kit for the detection of antibodies specific for HCV in a biological sample where said kit contains at least one purified and isolated peptide derived from the E1 or core cDNA sequences. In addition, the invention provides for a kit containing at least one purified and isolated peptide derived from the E1 cDNA sequences and at least one purified and isolated peptide derived from the core cDNA sequences.

The invention further provides isolated and purified genotype-specific oligonucleotides and analogs

° thereof derived from E1 and core cDNA sequences.

The invention also relates to methods for detecting the presence of hepatitis C virus in a mammal, said methods comprising analyzing the RNA of a mammal for the presence of hepatitis C virus. The invention further
5 relates to methods for determining the genotype of hepatitis C virus present in a mammal. This method is useful in determining the proper course of treatment for an HCV-infected patient.

The invention also provides a diagnostic kit for
10 the detection of hepatitis C virus in a biological sample. The kit comprises purified and isolated nucleic acid sequences useful as primers for reverse-transcription polymerase chain reaction (RT-PCR) analysis of RNA for the presence of hepatitis C virus genomic RNA.

The invention further provides a diagnostic kit
15 for the determination of the genotype of a hepatitis C virus present in a mammal. The kit comprises purified and isolated nucleic acid sequences useful as primers for RT-PCR analysis of RNA for the presence of HCV in a biological
20 sample and purified and isolated nucleic acid sequences useful as hybridization probes in determining the genotype of the HCV isolate detected in PCR analysis.

This invention also relates to pharmaceutical
25 compositions useful in prevention or treatment of hepatitis C in a mammal.

Description of Figures

Figures 1 A-H show computer generated sequence
alignments of the nucleotide sequences of 51 HCV E1 cDNAs.
30 The single letter abbreviations used for the nucleotides shown in Figures 1A-H are those standardly used in the art. Figure 1A shows the alignment of SEQ ID NOs:1-8 to produce a consensus sequence for genotype I/1a. Figure 1B shows the alignment of SEQ ID NOs:9-25 to produce a consensus
35 sequence for genotype II/1b. Figure 1C shows the alignment

° of SEQ ID NOs:26-29 to produce a consensus sequence for genotype III/2a. Figure 1D shows the alignment of SEQ ID NOs:30-33 to produce a consensus sequence for genotype IV/2b. Figure 1E shows the alignment of SEQ ID NOs:35-39 to produce a consensus sequence for genotype V/3a. Figure 1F shows the computer alignment of SEQ ID NOs:42-43 to produce a "consensus" sequence for genotype 4C where the "consensus" sequence given is that of SEQ ID NO:42. Figure 1G shows the alignment of SEQ ID NOs:45-50 to produce a consensus sequence for genotype 5a. The nucleotides shown in capital letters in the consensus sequences of Figures 1A-G are those conserved within a genotype while nucleotides shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 1A-E and 1G, when the lower case letter is shown in a consensus sequence, the lower case letter represents the nucleotide found most frequently in the sequences aligned to produce the consensus sequence. In Figure 1F, the lower case letters shown in the consensus sequence are nucleotides in SEQ ID NO:42 which differ from nucleotides found in the same positions in SEQ ID NO:43. Finally, a hyphen at a nucleotide position in the consensus sequences in Figures 1A-G indicates that two nucleotides were found in equal numbers at that position in the aligned sequences. In the aligned sequences, nucleotides are shown in lower case letters if they differed from the nucleotides of both adjacent isolates. Figure 1H shows the alignment of the consensus sequences of Figures 1A-G with SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ ID NO:51 (genotype 6a) to produce a consensus sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figure 1H where the nucleotides shown in capital letters are conserved among all genotypes and a blank space indicates that the nucleotide at that position is not conserved among all genotypes.

° Figures 2A-H show computer alignments of the deduced amino acid sequences of 51 HCV E1 cDNAs. The single letter abbreviations used for the amino acids shown in Figures 2A-H follow the conventional amino acid shorthand for the twenty naturally occurring amino acids.

5 Figure 2A shows the alignment of SEQ ID NOs:52-59 to produce a consensus sequence for genotype I/1a. Figure 2B shows the alignment of SEQ ID NOs:60-76 to produce a consensus sequence for genotype II/1b. Figure 2C shows the alignment of SEQ ID NOs:77-80 to produce a consensus

10 sequence for genotype III/2a. Figure 2D shows the alignment of SEQ ID NOs:81-84 to produce a consensus sequence for genotype IV/2b. Figure 2E shows the alignment of SEQ ID NOs:86-90 to produce a consensus sequence for genotype V/3a. Figure 2F shows the computer alignment of

15 SEQ ID NOs:93-94 to produce a consensus sequence for genotype 4c. Figure 2G shows the alignment of SEQ ID NOs:96-101 to produce a consensus sequence for genotype 5a. The amino acids shown in capital letters in the consensus sequences of Figures 2A-G are those conserved within a

20 genotype while amino acids shown in lower case letters in the consensus sequences are those variable within a genotype. In addition, in Figures 2A-E and 2G when the lower case letter is shown in a consensus sequence, the

25 letter represents the amino acid found most frequently in the sequences aligned to produce the consensus sequence. In Figure 2F, the lower case letters shown in the consensus sequence are amino acids in SEQ ID NO:93 which differ from amino acids found in the same positions in SEQ ID NO:94. Finally, a hyphen at an amino acid position in the

30 consensus sequences of Figures 2A-G indicates that two amino acids were found in equal numbers at that position in the aligned sequences. In the aligned sequences, amino acids are shown in lower case letters if they differed from the amino acids of both adjacent isolates. Figure 2H shows

35 the alignment of the consensus sequences of Figures 2A-G

° with SEQ ID NO:85 (genotype 2c), SEQ ID NO:91 (genotype 4a), SEQ ID NO:92 (genotype 4b), SEQ ID NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus sequence for all twelve genotypes. This consensus sequence is shown as the bottom line of Figure 2H where the amino acids shown in capital letters are conserved among all genotypes and a blank space indicates that the amino acid at that position is not conserved among all genotypes.

Figure 3 shows multiple sequence alignment of the deduced amino acid sequence of the E1 gene of 51 HCV isolates collected worldwide. The consensus sequence of the E1 protein is shown in boldface (top). In the consensus sequence cysteine residues are highlighted with stars, potential N-linked glycosylation sites are underlined, and invariant amino acids are capitalized, whereas variable amino acids are shown in lower case letters. In the alignment, amino acids are shown in lower case letters if they differed from the amino acid of both adjacent isolates. Amino acid residues shown in bold print in the alignment represent residues which at that position in the amino acid sequence are genotype-specific. Amino acids that were invariant among all HCV isolates are shown as hyphens (-) in the alignment. Amino acid positions correspond to those of the HCV prototype sequence (HCV-1, Choo, L. et al. (1991) Proc. Natl. Acad. Sci. USA 88:2451-2455) with the first amino acid of the E1 protein at position 192. The grouping of isolates into 12 genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a) is indicated.

Figure 4 shows a dendrogram of the genetic relatedness of the twelve genotypes of HCV based on the percent amino acid identity of the E1 gene of the HCV genome. The twelve genotypes shown are designated as I/1a, II/1b, III/2a, IV/2b, V/3a, 2c, 4a, 4b, 4c, 4d, 5a and 6a. The shaded bars represent a range showing the maximum and minimum homology between the amino acid sequence of any one

- ° isolate of the genotype indicated and the amino acid sequence of any other isolate.

Figure 5 shows the distribution of the complete E1 gene sequence of 74 HCV isolates into the twelve HCV genotypes in the 12 countries studied. For 51 of these HCV isolates, including 8 isolates of genotype I/1a, 17 isolates of genotype II/1b and 26 isolates comprising the additional 10 genotypes, the complete E1 gene sequence was determined. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on only a partial E1 gene sequence. The partially sequenced isolates did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. For ease of viewing, those genotypes designated by two terms (e.g., I/1a) are indicated by the latter term (e.g. 1a). The designations used for each country are: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z). National borders depicted in this figure represent those existing at the time of sampling.

Figures 6A-K show computer generated sequence alignments of the nucleotide sequences of 52 HCV core cDNAs. Single letter abbreviations used for the nucleotides shown in Figures 6A-J are those standardly used in the art. Figure 6A shows the alignment of SEQ ID NOS: 103-108 to produce a consensus sequence for genotype I/1a. Figure 6B shows the alignment of SEQ ID NOS: 109-124 to produce a consensus sequence for genotype II/1b. Figure 6C shows the alignments of the sequences comprising minor genotypes I/1a (SEQ ID NOS: 103-108) and II/1b (SEQ ID NOS: 109-124) to produce a consensus sequence for the major genotype, genotype 1. Figure 6D shows the alignment of SEQ ID NOS: 125-128 to produce a consensus sequence for genotype III/2a. Figure 6E shows the alignment of SEQ ID

° NOS: 129-133 to produce a consensus sequence for genotype IV/2b. Figure 6F shows the alignment of the sequences of minor genotypes III/2a (SEQ ID NOS: 125-128), IV/2b (SEQ ID NOS: 129-133) and 2c (SEQ ID NO: 134) to produce a consensus sequence for the major genotype, genotype 2.

5 Figure 6G shows the alignment of SEQ ID NOS: 135-138 to produce a consensus sequence for genotype V/3a. Figure 6H shows the computer alignment of the sequences of minor genotypes 4a-4f (SEQ ID NOS: 139-145) to produce a consensus sequence for the major genotype, genotype 4.

10 Figure 6I shows the alignment of SEQ ID NOS: 146-153 to produce a consensus sequence for genotype 5a. The nucleotides shown in capital letters in the consensus sequences in Figure 6A-I are those conserved within the genotype while nucleotides shown in lower case letters in the consensus sequences are those variable within a

15 genotype. In addition, when the lower case letter is shown in the consensus sequence, the lower case letter represents the nucleotide found most frequently in the sequences aligned to produce that consensus sequence. Moreover, a hyphen at a nucleotide position in the consensus sequences in Figures 6A-6I indicates that two nucleotides were found in equal numbers at that position in the sequences aligned to produce the consensus sequence. Finally, nucleotides are shown in lower case letters in the sequences aligned to

20 produce each consensus sequence shown in Figures 6A-6I, if they differed from the nucleotides of both adjacent isolates. Figure 6J shows the alignment of the consensus sequences of major genotypes 1 (Figure 6C), 2 (Figure 6F), 3 (Figure 6G), 4 (Figure 6H), 5 (Figure 6I) and 6 (SEQ ID NO: 154) to produce a consensus sequence for all genotypes

25 and Figure 6K shows the alignment of consensus sequences of Figures 6A, 6B, 6D, 6E, 6G and 6I with SEQ ID NO:134 (genotype 2c), SEQ ID NO:139 (genotype 4a), SEQ ID NO:141 (genotype 4b), SEQ ID NO:143 (genotype 4c), SEQ ID NO:145 (genotype 4d), SEQ ID NO:142 (genotype 4e), SEQ ID NO:140

30

35

° (genotype 4f) and SEQ ID NO:154 (genotype 6a) to produce a consensus sequence for all fourteen genotypes. The nucleotides shown in capital letters in the consensus sequences of Figures 6J and 6K are conserved among all genotypes and the nucleotide shown in lower case letter represent the nucleotides found most frequently in the sequences aligned to produce this consensus sequence. In addition, the presence of a hyphen at a nucleotide position in all fourteen sequences aligned in Figure 6K indicates that the nucleotide found at that position in the aligned sequences is the same as nucleotide shown at the corresponding position in the consensus sequences of Figure 6K.

Figures 7A-7J show computer alignments of the deduced amino acid sequences of the 52 HCV core cDNAs. The single letter abbreviations used for the amino acids shown in Figures 7A-7J follow the conventional amino acid shorthand for the twenty natural occurring amino acids. Figure 7A shows the alignment of SEQ ID NOS: 155-160 to produce a consensus sequence for genotype I/1a. Figure 7B shows the alignment of SEQ ID NOS: 161-176 to produce a consensus sequence for genotype II/1b. Figure 7C shows the alignment of the sequences comprising minor genotypes I/a (SEQ ID NOS: 155-160) and II/1b (SEQ ID NOS: 161-176) to produce a consensus sequence for the major genotype, genotype 1. Figure 7D shows the alignment of SEQ ID NOS: 177-180 to produce a consensus sequence for genotype III/2a. Figure 7E shows the alignment of SEQ ID NOS: 181-185 to produce a consensus sequence for genotype IV/2b. Figure 7F shows the alignment of the sequences of minor genotypes III/2a (SEQ ID NOS: 177-180), IV/2b (SEQ ID NOS: 181-185) and 2c (SEQ ID NO: 186) to produce a consensus sequence for the major genotype, genotype 2. Figure 7G shows the alignment of SEQ ID NOS: 187-190 to produce a consensus sequence for genotype V/3a. Figure 7H shows the computer alignment of the sequences of minor genotypes 4a-4f (SEQ ID NOS: 191-

197) to produce a consensus sequence for the major genotype, genotype 4. Figure 7I shows the alignment of SEQ ID NOs: 198-205 to produce a consensus sequence for genotype 5a. The amino acids shown in capital letters in the consensus sequences of Figures 7A-7I are those conserved within the genotype while amino acids shown in lower case letters in the consensus sequences are those variable within the genotype. In addition, when a lower case letter is found in the consensus sequences shown in Figures 7A-7I, the letter represents the amino acid found most frequently in the sequences aligned to produce that consensus sequence. Moreover, a hyphen in an amino acid position in the consensus sequences of Figures 7A-7I indicates that two amino acids were found in equal numbers at that position in the sequences aligned to produce that consensus sequence. Finally, amino acids are shown in lower case letters in the sequences aligned to produce the consensus sequences shown in Figures 7A-7I if these amino acids differed from the amino acids of both adjacent isolates. Figure 7J shows the alignment of the consensus sequences of major genotypes 1 (Figure 7C), 2 (Figure 7F), 3 (Figure 7G), 4 (Figure 7H), 5 (Figure 7I) and 6 (SEQ ID NO: 154) to produce a consensus sequence for all genotypes and Figure 7K shows the alignment of the consensus sequences of Figures 7A, 7B, 7D, 7E, 7G and 7I with SEQ ID NO:186 (genotype 2c), SEQ ID NO:191 (genotype 4a), SEQ ID NO:193 (genotype 4b), SEQ ID NO:195 (genotype 4c), SEQ ID NO:197 (genotype 4d), SEQ ID NO:194 (genotype 4e), SEQ ID NO:192 (genotype 4f) and SEQ ID NO:206 (genotype 6a) to produce a consensus sequence for all fourteen genotypes. The amino acids shown in capital letters in the consensus sequences shown in Figures 7J and 7K are conserved among all genotypes while the amino acids shown in lower case letters represent amino acids found most frequently in the sequences aligned to produce this consensus sequence. In addition, the presence of a hyphen at an amino acid

° position in all fourteen sequences aligned in Figure 7K indicates that the amino acid found at that position in the aligned sequences is the same as the amino acid shown at the corresponding position in the consensus sequence of Figure 7K.

5 Figure 8 shows phylogenetic trees illustrating the calculated evolutionary relationships of the different HCV isolates based upon the C gene sequence of 52 HCV isolates and the E1 gene sequence of 51 HCV isolates, respectively. The phylogenetic trees were constructed by
10 the unweighted pair-group method with arithmetic mean (Nei, M. (1987) *Molecular Evolutionary Genetics* (Columbia University Press, New York, N.Y.), pp 287-326) using the computer software package "Gene Works" from IntelliGenetics. The lengths of the horizontal lines
15 connecting the sequences, given in absolute values from 0 to 1, are proportional to the estimated genetic distances between the sequences. Genotype designations of HCV isolates are indicated. In 45 HCV isolates, both the C and the E1 gene sequences were determined.

20

Detailed Description Of Invention

The present invention relates to cDNAs encoding the complete nucleotide sequence of the envelope 1 (E1) and core genes of isolates of human hepatitis C virus (HCV).
25 The E1 cDNAs of the present invention were obtained as follows. Viral RNA was extracted from serum collected from humans infected with hepatitis C virus and the viral RNA was then reverse transcribed and amplified by polymerase chain reaction using primers deduced from the sequence of
30 the HCV strain H-77 (Ogata, N. et al. (1991) *Proc. Natl. Acad. Sci. U.S.A.* 88:3392-3396). The amplified cDNA was then isolated by gel electrophoresis and sequenced.

The present invention further relates to the nucleotide sequences of the cDNAs encoding the E1 gene of
35 51 HCV isolates. These nucleotide sequences are shown in

° the sequence listing as SEQ ID NO:1 through SEQ ID NO:51.

The abbreviations used for the nucleotides are those standardly used in the art.

The deduced amino acid sequence of each of SEQ ID NO:1 through SEQ ID NO:51 are presented in the sequence listing as SEQ ID NO:52 through SEQ ID NO:102 where the amino acid sequence in SEQ ID NO:52 is deduced from the nucleotide sequence shown in SEQ ID NO:1, the amino acid sequence shown in SEQ ID NO:53 is deduced from the nucleotide sequence shown in SEQ ID NO:2 and so on. The deduced amino acid sequence of each of SEQ ID Nos:52-102 starts at nucleotide 1 of the corresponding nucleic acid sequence shown in SEQ ID Nos:1-51 and extends 575 nucleotides to a total length of 576 nucleotides.

The three letter abbreviations used in SEQ ID Nos:52-102 follow the conventional amino acid shorthand for the twenty naturally occurring amino acids.

The present invention also relates to the nucleotide sequences of the cDNAs encoding the core gene of 52 HCV isolates. These nucleotide sequences are shown in the sequence listing as SEQ ID NO:103 through SEQ ID NO:154.

The core cDNAs of the present invention were obtained as follows. Viral RNA was extracted from serum and reversed transcribed as described above for cloning of the E1 cDNAs. The core cDNAs of the present invention were then amplified by polymerase chain reaction using primers deduced from previously determined sequences that flank the core gene (Bukh et al. (1992)) Proc. Natl. Acad. Sci. U.S.A., 89: 4942-4946; Bukh et al. (1993) Proc. Natl. Acad. Sci. U.S.A., 90: 8234-8238).

The deduced amino acid sequence of each of SEQ ID NO:103 through SEQ ID NO:154 are presented in the sequence listing as SEQ ID NO:155 through SEQ ID NO:206 where the amino acid sequence in SEQ ID NO:155 is deduced from the nucleotide sequence shown in SEQ ID NO:103, the amino acid

° sequence shown in SEQ ID NO:156 is deduced from the nucleotide sequence shown in SEQ ID NO:104 and so on. The deduced amino acid sequence of each of SEQ ID NOs: 155-206 starts at nucleotide 1 of the corresponding nucleotide sequence shown in SEQ ID NOs:103-154 and extends 572
5 nucleotides to a total length of 573 nucleotides.

Preferably, the E1 and core proteins and peptides of the present invention are substantially homologous to, and most preferably biologically equivalent to, native HCV E1 and core proteins and peptides. By "biologically
10 equivalent" as used throughout the specification and claims, it is meant that the compositions are immunogenically equivalent to the native E1 and core proteins and peptides. The E1 and core proteins and peptides of the present invention may also stimulate the
15 production of protective antibodies upon injection into a mammal that would serve to protect the mammal upon challenge with HCV. By "substantially homologous" as used throughout the ensuing specification and claims to describe E1 and core proteins and peptides, it is meant a degree of
20 homology in the amino acid sequence of the E1 and core proteins and peptides to the native E1 and core proteins and peptides respectively. Preferably the degree of homology is in excess of 90, preferably in excess of 95, with a particularly preferred group of proteins being in
25 excess of 99 homologous with the native E1 or core proteins and peptides.

Variations are contemplated in the cDNA sequences shown in SEQ ID NO:1 through SEQ ID NO:51 and in SEQ ID NO:103 through SEQ ID NO:154 which will result in a nucleic
30 acid sequence that is capable of directing production of analogs of the corresponding protein shown in SEQ ID NO:52 through SEQ ID NO:102 and in SEQ ID NO:155 through SEQ ID NO:206. It should be noted that the cDNA sequences set forth above represent a preferred embodiment of the present
35 invention. Due to the degeneracy of the genetic code, it

° is to be understood that numerous choices of nucleotides may be made that will lead to a DNA sequence capable of directing production of the instant protein or its analogs. As such, DNA sequences which are functionally equivalent to the sequence set forth above or which are functionally equivalent to sequences that would direct production of analogs of the E1 and core proteins produced pursuant to the amino acid sequences set forth above, are intended to be encompassed within the present invention.

The term analog as used throughout the specification or claims to describe the E1 and core proteins and peptides of the present invention, includes any protein or peptide having an amino acid residue sequence substantially identical to a sequence specifically shown herein in which one or more residues have been conservatively substituted with a biologically equivalent residue. Examples of conservative substitutions include the substitution of one polar (hydrophobic) residue such as isoleucine, valine, leucine or methionine for another, the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, between glycine and serine, the substitution of one basic residue such as lysine, arginine or histidine for another, or the substitution of one acidic residue, such as aspartic acid or glutamic acid for another.

The phrase "conservative substitution" also includes the use of a chemically derivatized residue in place of a non-derivatized residue provided that the resulting protein or peptide is biologically equivalent to the native E1 or core protein or peptide.

"Chemical derivative" refers to an E1 or core protein or peptide having one or more residues chemically derivatized by reaction of a functional side group. Examples of such derivatized molecules, include but are not limited to, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene

° sulfonyl groups, carbobenzoxy groups, t-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-imbenzylhistidine. Also included as chemical derivatives are those proteins or peptides which contain one or more naturally-occurring amino acid derivatives of the twenty standard amino acids. For examples: 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine. The E1 and core proteins and peptide of the present invention also includes any protein or peptide having one or more additions and/or deletions of residues relative to the sequence of a peptide whose sequence is shown herein, so long as the peptide is biologically equivalent to the native E1 or core protein or peptide.

20 The present invention also includes a recombinant DNA method for the manufacture of HCV E1 and core proteins. In this method, natural or synthetic nucleic acid sequences may be used to direct the production of E1 and core proteins.

25 In one embodiment of the invention, the method comprises:

(a) preparation of a nucleic acid sequence capable of directing a host organism to produce HCV E1 or core protein;

30 (b) cloning the nucleic acid sequence into a vector capable of being transferred into and replicated in a host organism, such vector containing operational elements for the nucleic acid sequence;

35 (c) transferring the vector containing the

- ° nucleic acid and operational elements into a host organism capable of expressing the protein;
- (d) culturing the host organism under conditions appropriate for amplification of the vector and expression of the protein; and
- 5 (e) harvesting the protein.

In another embodiment of the invention, the method for the recombinant DNA synthesis of an HCV E1 protein encoded by any one of the nucleic acid sequences shown in SEQ ID NOS:1-51 comprises:

- 10 (a) culturing a transformed or transfected host organism containing a nucleic acid sequence capable of directing the host organism to produce a protein, under conditions such that the protein is produced, said protein exhibiting substantial homology to a native E1 protein
- 15 isolated from HCV having the amino acid sequence according to any one of the amino acid sequences shown in SEQ ID NOS:52-102 or combinations thereof.

- In one embodiment, the RNA sequence of an HCV isolate was isolated and converted to cDNA as follows.
- 20 Viral RNA is extracted from a biological sample collected from human subjects infected with hepatitis C and the viral RNA is then reverse transcribed and amplified by polymerase chain reaction using primers deduced from the sequence of HCV strain H-77 (Ogata et al. (1991)). Preferred primer
 - 25 sequences are shown as SEQ ID NOS:207-212 in the sequence listing. Once amplified, the PCR fragments are isolated by gel electrophoresis and sequenced.

- In an alternative embodiment, the above method may be utilized for the recombinant DNA synthesis of an HCV
- 30 core protein encoded by any one of the nucleic acid sequences shown in SEQ ID NOS: 103-154, where the protein produced by this method exhibits substantial homology to a native core protein isolated from HCV having amino acid sequence according to any one of the amino acid sequences
 - 35 shown in SEQ ID NOS: 155-206 or combinations thereof.

° The vectors contemplated for use in the present invention include any vectors into which a nucleic acid sequence as described above can be inserted, along with any preferred or required operational elements, and which vector can then be subsequently transferred into a host organism and replicated in such organisms. Preferred vectors are those whose restriction sites have been well documented and which contain the operational elements preferred or required for transcription of the nucleic acid sequence.

10 The "operational elements" as discussed herein include at least one promoter, at least one operator, at least one leader sequence, at least one terminator codon, and any other DNA sequences necessary or preferred for appropriate transcription and subsequent translation of the vector nucleic acid. In particular, it is contemplated
15 that such vectors will contain at least one origin of replication recognized by the host organism along with at least one selectable marker and at least one promoter sequence capable of initiating transcription of the nucleic acid sequence.

20 In construction of the recombinant expression vectors of the present invention, it should additionally be noted that multiple copies of the nucleic acid sequence of interest (either E1 or core) and its attendant operational elements may be inserted into each vector. In such an embodiment, the host organism would produce greater amounts per vector of the desired E1 or core protein. The number of multiple copies of the nucleic acid sequence which may be inserted into the vector is limited only by the ability
25 of the resultant vector due to its size, to be transferred into and replicated and transcribed in an appropriate host microorganism.

30 Of course, those skilled in the art would readily understand that copies of both core and E1 nucleic acid sequence may be inserted into single vector such that a
35

° host organism transformed or transfected with said vector would produce both the desired E1 and core proteins. For example, a polysistronic vector in which multiple different E1 and/or core proteins may be expressed from a single vector is created by placing expression of each protein under control of an internal ribosomal entry site (IRES) (Molla, A. et al. Nature, 356:255-257 (1992); Gong, S.K. et al. J. of Virol., 263:1651-1660 (1989)).

In another embodiment, restriction digest fragments containing a coding sequence for E1 or core proteins can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells. By suitable is meant that the vector is capable of carrying and expressing a complete nucleic acid sequence coding for an E1 or core protein. Preferred expression vectors are those that function in a eukaryotic cell. Examples of such vectors include but are not limited to vaccinia virus vectors, adenovirus or herpes viruses. A preferred vector is the baculovirus transfer vector, pBlueBac.

In yet another embodiment, the selected recombinant expression vector may then be transfected into a suitable eukaryotic cell system for purposes of expressing the recombinant protein. Such eukaryotic cell systems include but are not limited to cell lines such as HeLa, MRC-5 or CV-1. A preferred eukaryotic cell system is SF9 insect cells.

The expressed recombinant protein may be detected by methods known in the art including, but not limited to, Coomassie blue staining and Western blotting.

The present invention also relates to substantially purified and isolated recombinant E1 and core proteins. In one embodiment, the recombinant protein expressed by the SF9 cells can be obtained as a crude lysate or it can be purified by standard protein purification procedures known in the art which may include differential precipitation, molecular sieve chromatography,

- ° ion-exchange chromatography, isoelectric focusing, gel electrophoresis and affinity and immunoaffinity chromatography. The recombinant protein may be purified by passage through a column containing a resin which has bound thereto antibodies specific for the open reading frame (ORF) protein.

5 The present invention further relates to the use of recombinant E1 and core proteins as diagnostic agents and vaccines. In one embodiment, the expressed recombinant proteins of this invention can be used in immunoassays for
10 diagnosing or prognosing hepatitis C in a mammal. For the purposes of the present invention, "mammal" as used throughout the specification and claims, includes, but is not limited to humans, chimpanzees, other primates and the like. In a preferred embodiment, the immunoassay is useful
15 in diagnosing hepatitis C infection in humans.

Immunoassays of the present invention may be those commonly used by those skilled in the art including, but not limited to, radioimmunoassay, Western blot assay, immunofluorescent assay, enzyme immunoassay,
20 chemiluminescent assay, immunohistochemical assay, immunoprecipitation and the like. Standard techniques known in the art for ELISA are described in Methods in Immunodiagnosis, 2nd Edition, Rose and Bigazzi, eds., John Wiley and Sons, 1980 and Campbell et al., Methods of Immunology, W.A. Benjamin, Inc., 1964, both of which are
25 incorporated herein by reference. Such assays may be a direct, indirect, competitive, or noncompetitive immunoassay as described in the art (Oellerich, M. 1984. J. Clin. Chem. Clin. BioChem 22:895-904) Biological samples appropriate for such detection assays include, but are not
30 limited to serum, liver, saliva, lymphocytes or other mononuclear cells.

In a preferred embodiment, test serum is reacted with a solid phase reagent having surface-bound recombinant HCV E1 and/or core protein(s) as antigen(s). The solid
35

° surface reagent can be prepared by known techniques for attaching protein to solid support material. These attachment methods include non-specific adsorption of the protein to the support or covalent attachment of the protein to a reactive group on the support. After reaction of the antigen with anti-HCV antibody, unbound serum components are removed by washing and the antigen-antibody complex is reacted with a secondary antibody such as labelled anti-human antibody. The label may be an enzyme which is detected by incubating the solid support in the presence of a suitable fluorimetric or calorimetric reagent. Other detectable labels may also be used, such as radiolabels or colloidal gold, and the like.

The HCV E1 and/or core proteins and analogs thereof may be prepared in the form of a kit, alone, or in combinations with other reagents such as secondary antibodies, for use in immunoassays.

In yet another embodiment the recombinant E1 and core proteins or analogs thereof can be used as a vaccine to protect mammals against challenge with hepatitis C. The vaccine, which acts as an immunogen, may be a cell, cell lysate from cells transfected with a recombinant expression vector or a culture supernatant containing the expressed protein. Alternatively, the immunogen is a partially or substantially purified recombinant protein. In yet another embodiment, the immunogen may be a fusion protein comprising core protein and a second, non-core protein joined together such that the core portion of the fusion protein will aggregate and "trap" the second protein on the surface of the particle produced by aggregation of the core protein. (Molecular Biology of the Hepatitis B Virus", McLachlan, A. (1991) CRC Press, Boca Raton, Fla.). Alternatively, the core protein could be mixed with the second protein in vitro to produce particles in which all or part of the second protein was exposed on the surface of the particle. Such particles would then serve as a carrier

° in a multi-valent vaccine preparation. Second proteins or parts thereof which could be mixed with or fused to the core protein include, but are not limited to, HCV E1 and hepatitis B surface antigen.

While it is possible for the immunogen to be
5 administered in a pure or substantially pure form, it is preferable to present it as a pharmaceutical composition, formulation or preparation.

The formulations of the present invention, both for veterinary and for human use, comprise an immunogen as
10 described above, together with one or more pharmaceutically acceptable carriers and optionally other therapeutic ingredients. The carrier(s) must be "acceptable" in the sense of being compatible with the other ingredients of the formulation and not deleterious to the recipient thereof.
15 The formulations may conveniently be presented in unit dosage form and may be prepared by any method well-known in the pharmaceutical art.

All methods include the step of bringing into association the active ingredient with the carrier which
20 constitutes one or more accessory ingredients. In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product into the desired
25 formulation.

Formulations suitable for intravenous intramuscular, subcutaneous, or intraperitoneal administration conveniently comprise sterile aqueous solutions of the active ingredient with solutions which are
30 preferably isotonic with the blood of the recipient. Such formulations may be conveniently prepared by dissolving the solid active ingredient in water containing physiologically compatible substances such as sodium chloride (e.g. 0.1-2.0m), glycine, and the like, and having a buffered pH
35 compatible with physiological conditions to produce an

° aqueous solution, and rendering said solution sterile. These may be present in unit or multi-dose containers, for example, sealed ampules or vials.

The formulations of the present invention may incorporate a stabilizer. Illustrative stabilizers are preferably incorporated in an amount of 0.10-10,000 parts by weight per part by weight of immunogens. If two or more stabilizers are to be used, their total amount is preferably within the range specified above. These stabilizers are used in aqueous solutions at the appropriate concentration and pH. The specific osmotic pressure of such aqueous solutions is generally in the range of 0.1-3.0 osmoles, preferably in the range of 0.8-1.2. The pH of the aqueous solution is adjusted to be within the range of 5.0-9.0, preferably within the range of 6-8. In formulating the immunogen of the present invention, an anti-adsorption agent may be used.

Additional pharmaceutical methods may be employed to control the duration of action. Controlled release preparations may be achieved through the use of polymer to complex or adsorb the proteins or their derivatives. The controlled delivery may be exercised by selecting appropriate macromolecules (for example polyester, polyamino acids, polyvinyl pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine sulfate) and the concentration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled-release preparations is to incorporate the proteins, protein analogs or their functional derivatives, into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules

° prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly (methylmethacrylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, 5 albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions.

When oral preparations are desired, the compositions may be combined with typical carriers, such as lactose, sucrose, starch, talc, magnesium stearate, 10 crystalline cellulose, methyl cellulose, carboxymethyl cellulose, glycerin, sodium alginate or gum arabic among others.

The E1 and core proteins of the present invention may also be used as a delivery system for anti-virals to prevent or attenuate HCV infection in a mammal by utilizing 15 the property of both proteins to self-aggregate in vitro to "trap" the antiviral within the particles produced via aggregation of the core and E1 proteins. Examples of anti-virals which could be delivered by such a system include, 20 but are not limited to antisense DNA or RNAs.

Vaccination can be conducted by conventional methods. For example, the immunogen or immunogens (e.g. the E1 protein may be administered alone or in combination with the E1 proteins derived from other isolates of HCV) 25 can be used in a suitable diluent such as saline or water, or complete or incomplete adjuvants. Further, the immunogen(s) may or may not be bound to a carrier to make the protein(s) immunogenic. Examples of such carrier molecules include but are not limited to bovine serum 30 albumin (BSA), keyhole limpet hemocyanin (KLH), tetanus toxoid, and the like. The immunogen(s) can be administered by any route appropriate for antibody production such as intravenous, intraperitoneal, intramuscular, subcutaneous, and the like. The immunogen(s) may be administered once or 35 at periodic intervals until a significant titer of anti-HCV

- ° antibody is produced. The antibody may be detected in the serum using an immunoassay.

In yet another embodiment, the immunogen may be nucleic acid sequence capable of directing host organism synthesis of E1 and/or core protein(s). Such nucleic acid sequence may be inserted into a suitable expression vector by methods known to those skilled in the art. Expression vectors suitable for producing high efficiency gene transfer in vivo include retroviral, adenoviral and vaccinia viral vectors. Operational elements of such expression vectors are disclosed previously in the present specification and are known to one skilled in the art. Such expression vectors can be administered intravenously, intramuscularly, subcutaneously, intraperitoneally or orally.

In an alternative embodiment, direct gene transfer may be accomplished via intramuscular injection of, for example, plasmid-based eukaryotic expression vectors containing a nucleic acid sequence capable of directing host organism synthesis of E1 and/or core protein(s). Such an approach has previously been utilized to produce the hepatitis B surface antigen in vivo and resulted in an antibody response to the surface antigen (Davis, H.L. et al. (1993) Human molecular Genetics, 2:1847-1851; see also Davis et al. (1993) Human Gene Therapy, 4:151-159 and 733-740).

Doses of E1 and/or core protein(s)-encoding nucleic acid sequence effective to elicit a protective antibody response against HCV infection range from about 1 to about 500 μ g. A more preferred range being about 1 to about 500 μ g.

The E1 and/or core proteins and expression vectors containing a nucleic acid sequence capable of directing host organism synthesis of E1 and/or core protein(s) may be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described

° above.

The administration of the immunogen(s) of the present invention may be for either a prophylactic or therapeutic purpose. When provided prophylactically, the immunogen(s) is provided in advance of any exposure to HCV or in advance of any symptom of any symptoms due to HCV infection. The prophylactic administration of the immunogen serves to prevent or attenuate any subsequent infection of HCV in a mammal. When provided therapeutically, the immunogen(s) is provided at (or shortly after) the onset of the infection or at the onset of any symptom of infection or disease caused by HCV. The therapeutic administration of the immunogen(s) serves to attenuate the infection or disease.

In addition to use as a vaccine, the compositions can be used to prepare antibodies to HCV E1 and core proteins. The antibodies can be used directly as antiviral agents or they may be used in immunoassays disclosed herein to detect HCV E1 and core proteins present in patient sera.. To prepare antibodies, a host animal is immunized using the E1 and/or core proteins native to the virus particle bound to a carrier as described above for vaccines. The host serum or plasma is collected following an appropriate time interval to provide a composition comprising antibodies reactive with the E1 or core protein of the virus particle. The gamma globulin fraction or the IgG antibodies can be obtained, for example, by use of saturated ammonium sulfate or DEAE Sephadex, or other techniques known to those skilled in the art. The antibodies are substantially free of many of the adverse side effects which may be associated with other anti-viral agents such as drugs.

The antibody compositions can be made even more compatible with the host system by minimizing potential adverse immune system responses. This is accomplished by removing all or a portion of the Fc portion of a foreign

° species antibody or using an antibody of the same species as the host animal, for example, the use of antibodies from human/human hybridomas. Humanized antibodies (i.e., nonimmunogenic in a human) may be produced, for example, by replacing an immunogenic portion of an antibody with a
5 corresponding, but nonimmunogenic portion (i.e., chimeric antibodies). Such chimeric antibodies may contain the reactive or antigen-binding portion of an antibody from one species and the Fc portion of an antibody (nonimmunogenic) from a different species. Examples of chimeric antibodies,
10 include but are not limited to, non-human mammal-human chimeras, rodent-human chimeras, murine-human and rat-human chimeras (Robinson et al., International Patent Application 184,187; Taniguchi M., European Patent Application 171,496; Morrison et al., European Patent Application 173,494;
15 Neuberger et al., PCT Application WO 86/01533; Cabilly et al., 1987 Proc. Natl. Acad. Sci. USA 84:3439; Nishimura et al., 1987 Canc. Res. 47:999; Wood et al., 1985 Nature 314:446; Shaw et al., 1988 J. Natl. Cancer Inst. 80:15553, all incorporated herein by reference).

20 General reviews of "humanized" chimeric antibodies are provided by Morrison S., 1985 Science 229:1202 and by Oi et al., 1986 BioTechniques 4:214.

Suitable "humanized" antibodies can be alternatively produced by CDR or CEA substitution (Jones et
25 al., 1986 Nature 321:552; Verhoeyan et al., 1988 Science 239:1534; Biedler et al. 1988 J. Immunol. 141:4053, all incorporated herein by reference).

The antibodies or antigen binding fragments may also be produced by genetic engineering. The technology
30 for expression of both heavy and light chain genes in E. coli is the subject of the PCT patent applications; publication number WO 901443, WO901443, and WO 9014424 and in Huse et al., 1989 Science 246:1275-1281.

The antibodies can also be used as a means of enhancing the immune response. The antibodies can be
35

° administered in amount similar to those used for other therapeutic administrations of antibody. For example, normal immune globulin is administered at 0.02-0.1 ml/lb body weight during the early incubation period of other viral diseases such as rabies, measles, and hepatitis B to interfere with viral entry into cells. Thus, antibodies reactive with the HCV E1 and/or core proteins can be passively administered alone or in conjunction with another anti-viral agent to a host infected with an HCV to enhance the immune response and/or the effectiveness of an antiviral drug.

Alternatively, anti-HCV E1 antibodies and anti-HCV core antibodies can be induced by administered anti-idiotypic antibodies as immunogens. Conveniently, a purified anti-HCV E1 or anti-HCV core antibody preparation prepared as described above is used to induce anti-idiotypic antibody in a host animal, the composition is administered to the host animal in a suitable diluent. Following administration, usually repeated administration, the host produces anti-idiotypic antibody. To eliminate an immunogenic response to the Fc region, antibodies produced by the same species as the host animal can be used or the Fc region of the administered antibodies can be removed. Following induction of anti-idiotypic antibody in the host animal, serum or plasma is removed to provide an antibody composition. The composition can be purified as described above for anti-HCV E1 and anti-HCV core antibodies, or by affinity chromatography using anti-HCV E1 or anti-HCV core antibodies bound to the affinity matrix. The anti-idiotypic antibodies produced are similar in conformation to the authentic HCV E1 or core protein and may be used to prepare an HCV vaccine rather than using an HCV E1 or core protein.

When used as a means of inducing anti-HCV virus antibodies in an animal, the manner of injecting the antibody is the same as for vaccination purposes, namely intramuscularly, intraperitoneally, subcutaneously or the

- ° like in an effective concentration in a physiologically suitable diluent with or without adjuvant. One or more booster injections may be desirable.

The HCV E1 and core proteins of the invention are also intended for use in producing antiserum designed for pre- or post-exposure prophylaxis. Here an E1 or core protein, or mixture of E1 and/or core proteins is formulated with a suitable adjuvant and administered by injection to human volunteers, according to known methods for producing human antisera. Antibody response to the injected proteins is monitored, during a several-week period following immunization, by periodic serum sampling to detect the presence of anti-HCV E1 and/or anti-HCV core serum antibodies, using an immunoassay as described herein.

The antiserum from immunized individuals may be administered as a pre-exposure prophylactic measure for individuals who are at risk of contracting infection. The antiserum is also useful in treating an individual post-exposure, analogous to the use of high titer antiserum against hepatitis B virus for post-exposure prophylaxis.

For both in vivo use of antibodies to HCV virus-like particles and proteins and anti-idiotypic antibodies and diagnostic use, it may be preferable to use monoclonal antibodies. Monoclonal anti-HCV E1 and anti-HCV core protein antibodies or anti-idiotypic antibodies can be produced as follows. The spleen or lymphocytes from an immunized animal are removed and immortalized or used to prepare hybridomas by methods known to those skilled in the art. (Goding, J.W. 1983. Monoclonal Antibodies: Principles and Practice, Pladermic Press, Inc., NY, NY, pp. 56-97). To produce a human-human hybridoma, a human lymphocyte donor is selected. A donor known to be infected with HCV (where infection has been shown for example by the presence of anti-virus antibodies in the blood or by virus culture) may serve as a suitable lymphocyte donor. Lymphocytes can be isolated from a peripheral blood sample

° or spleen cells may be used if the donor is subject to splenectomy. Epstein-Barr virus (EBV) can be used to immortalize human lymphocytes or a human fusion partner can be used to produce human-human hybridomas. Primary in vitro immunization with peptides can also be used in the generation of human monoclonal antibodies.

Antibodies secreted by the immortalized cells are screened to determine the clones that secrete antibodies of the desired specificity. For monoclonal anti-E1 and anti-core antibodies, the antibodies must bind to HCV E1 and core proteins respectively. For monoclonal anti-idiotypic antibodies, the antibodies must bind to anti-E1 and anti-core protein antibodies respectively. Cells producing antibodies of the desired specificity are selected.

The present invention also relates to the use of single-stranded antisense poly- or oligonucleotides derived from nucleotide sequences substantially homologous to those shown in SEQ ID NOs:1-51 to inhibit the expression of hepatitis C E1 genes. The present invention further relates to the use of single-stranded anti-sense poly- or oligo-nucleotides derived from nucleotide sequences substantially homologous to those shown in SEQ ID NOs:103-154 to inhibit the expression of hepatitis C core genes. Alternatively, the anti-sense poly- or oligo-nucleotides may be complementary to both the E1 and core genes and hence, inhibit the expression of both hepatitis C E1 and core genes. By substantially homologous as used throughout the specification and claims to describe the nucleic acid sequences of the present invention, is meant a level of homology between the nucleic acid sequence and the SEQ ID NOs. referred to in the above sentence. Preferably, the level of homology is in excess of 80%, more preferably in excess of 90%, with a preferred nucleic acid sequence being in excess of 95% homologous with the DNA sequence shown in the indicated SEQ ID NO. These anti-sense poly- or oligonucleotides can be either DNA or RNA. The targeted

° sequence is typically messenger RNA and more preferably, a single sequence required for processing or translation of the RNA. The anti-sense poly- or oligonucleotides can be conjugated to a polycation such as polylysine as disclosed in Lemaitre, M. et al. ((1989) Proc. Natl. Acad. Sci. USA 84:648-652) and this conjugate can be administered to a mammal in an amount sufficient to hybridize to and inhibit the function of the messenger RNA.

10 The present invention further relates to multiple computer-generated alignments of the nucleotide and deduced amino acid sequences shown in SEQ ID NOs:1-206. Computer analysis of the nucleotide sequences shown in SEQ ID NOs:1-51 and 103-154 and of the deduced amino acid sequences shown in SEQ ID NOs:52-102 and 155-206 can be carried out using commercially available computer programs known to one skilled in the art.

15 In one embodiment, computer analysis of SEQ ID NOs:1-51 by the program GENALIGN (Intelligenetics, Inc. Mountainview, CA) results in distribution of the 51 HCV E1 sequences into twelve genotypes based upon the degree of variation of the sequences. For the purposes of the present invention, the nucleotide sequence identity of E1 cDNAs of HCV isolates of the same genotype is in the range of about 85% to about 100% whereas the identity of E1 cDNA sequences of different genotypes is in the range of about 20 50% to about 80%.

25 The grouping of SEQ ID NOs:1-51 into twelve HCV genotypes is shown below.

30

35

	<u>SEQ ID NOs:</u>	<u>Genotypes</u>
	1-8	I/1a
	9-25	II/1b
	26-29	III/2a
	30-33	IV/2b
	34	2c
5	35-39	V/3a
	40	4a
	41	4b
	42-43	4c
	44	4d
	45-50	5a
	51	6a

10 For those genotypes containing more than one E1 nucleotide sequence, computer alignment of the constituent nucleotide sequences of the genotype was conducted using GENALIGN in order to produce a consensus sequence for each genotype. These alignments and their resultant consensus sequences are shown in Figures 1A-G for the seven genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which comprise more than one nucleotide sequence. Further alignment of the consensus sequences of Figures 1A-G with SEQ ID NO:34 (genotype 2c), SEQ ID NO:40 (genotype 4a), SEQ ID NO:41 (genotype 4b), SEQ ID NO:44 (genotype 4d) and SEQ ID NO:51 (genotype 6a) produces a consensus sequence for all twelve genotypes as shown in Figure 1H. The multiple alignments of nucleotide sequences shown in Figures 1A-H produce consensus sequences which serve to highlight regions of homology and non-homology between sequences found within the same genotype or in different genotypes and hence, these alignments can be used by one skilled in the art to design oligonucleotides useful as reagents in diagnostic assays for HCV.

30 Examples of purified and isolated oligonucleotide sequences derived from the consensus sequences shown in Figures 1A-H include, but are not limited to, SEQ ID NOs:213-239 where these oligonucleotides are useful as "genotype-specific" primers and probes since these

35

oligonucleotides can hybridize specifically to the nucleotide sequence of the E1 gene of HCV isolates belonging to a single genotype. The genotype-specificity of the oligonucleotides shown in SEQ ID NOS:213-239 is as follows: SEQ ID NOS:213-214 are specific for genotype I/1a; SEQ ID NOS:215-216 are specific for genotype II/1b; SEQ ID NOS:217-218 are specific for genotype III/2a; SEQ ID NOS:219-220 are specific for genotype IV/2b; SEQ ID NOS:221-223 are specific for genotype 2c; SEQ ID NOS:224-226 are specific for genotype V/3a; SEQ ID NOS:227-228 are specific for genotype 4a; SEQ ID NOS:229-230 are specific for genotype 4b; SEQ ID NOS:231-232 are specific for genotype 4c; SEQ ID NOS:233-234 are specific for genotype 4d; SEQ ID NOS:235-236 are specific for genotype 5a and SEQ ID NOS:237-239 are specific for genotype 6a.

In another embodiment, the computer analysis of SEQ ID NOS:103-154 by the program GENALIGN results in distribution of the 52 HCV core sequences into 14 genotypes based upon the degree of variation of the sequences.

The grouping of SEQ ID NOS:103-154 into 14 HCV genotypes is shown below.

	<u>SEQ ID NOS:</u>	<u>Genotypes</u>
	103-108	I/1a
	109-124	II/1b
	125-128	III/2a
	129-133	IV/2b
	134	2c
	135-138	V/3a
	139	4a
	141	4b
	143	4c
	144	4c
	145	4d
	142	4e
	140	4f
	146-153	5a
	154	6a

These 14 genotypes can be further grouped into 6

major genotypes designated genotypes 1-6 where genotype 1 comprises the sequences contained in minor genotypes I/1a and II/1b; genotype 2 comprises the sequences contained in minor genotypes III/2a, IV/2b and 2c; genotype 3 comprises sequences contained in genotype V/3a; genotype 4 comprises sequences contained in minor genotypes 4a-4f; genotype 5 comprises the sequences contained in genotype 5a and genotype 6 comprises the sequence contained in genotype 6a. Computer alignment of the constituent nucleotide sequences of the core cDNAs falling within genotypes I/1a, II/1b, III/2a, IV/2b, V/3a and 5a, to produce a consensus sequence for each of these genotypes is shown in Figures 6A (I/1a), 6B (II/1b), 6D (III/2a), 6E (IV/2b), 6G (V/3a) and 6I (5a). The alignment of the sequences found in minor genotypes I/1a and II/1b to produce a consensus sequence for major genotype 1 is shown in Figure 6C. The alignment of the sequences contained in minor genotypes III/2a, IV/2b and 2c to produce a consensus sequence for major genotype 2 is shown in Figure 6F. The alignment of the nucleotide sequences contained in minor genotypes 4a-4f to produce a consensus sequence for major genotype 4 is shown in Figure 6H. Further alignment of the consensus sequences shown in Figures 6C, 6F, 6G, 6H and 6I with SEQ ID NO:154 (genotype 6a/major genotype 6) to produce a consensus sequence for all genotypes is shown in Figure 6J and alignment of the consensus sequences shown in Figures 6A, 6B, 6D, 6E, 6G and 6I with 4a), SEQ ID NO:141 (genotype 4b), SEQ ID NO:143 (genotype 4c), SEQ ID NO:145 (genotype 4d), SEQ ID NO:142 (genotype 4e), SEQ ID NO:140 (genotype 4f) and SEQ ID NO:154 (genotype 6a) to produce a consensus sequence for all fourteen genotypes is shown in Figure 6K. As with the alignments of the envelope (E1) nucleotide sequences, the consensus sequences shown in Figures 6A-6K serve to highlight regions of homology and non-homology between sequences found within the same genotype or in different genotypes and hence, can be used by one skilled in the art

- ° to design oligonucleotides useful as reagents in diagnostic assays for HCV.

For example, purified and isolated oligonucleotide sequences derived from the consensus sequences shown in Figures 6A-6K may be useful as genotype-specific primers and probes since these oligonucleotides can hybridize specifically to the nucleotide sequence of the core gene of HCV isolates belonging to a given genotype. Examples of regions of the consensus sequence of the core gene of a given genotype from which primers specific for that genotype may be deduced include but are not limited to, the nucleotide domains shown below for each genotype. The sequence in which the indicated nucleotide domains are found are indicated in parentheses to the right of each genotype.

15 Genotype 1 (Consensus Sequence of Figure 6C)

427-466, 444-483, 447-486 (5'-3', sense)

505-466, 522-483, 525-486 (5'-3', antisense)

20 Genotype 1a (Consensus Sequence of Figure 6A)

141-180, 279-318 (5'-3', sense)

219-180, 246-207 (5'-3', antisense)

25 Genotype 1b (Consensus Sequence of Figure 6B)

67-106, 127-186, 234-273 (5'-3', sense)

144-106, 225-186, 311-272, 312-273 (5'-3', antisense)

30 Genotype 2 (Consensus Sequence of Figure 6F)

153-192, 162-201, 164-203, 168-207, 171-210, 182-221, 192-231, 193-232, 302-341 (5'-3', sense)

231-192, 240-201, 242-203, 246-207, 249-210, 260-221, 270-231, 271-232, 380-341 (5'-3', antisense)

35 Genotype III/2a (Consensus Sequence of Figure 6D)

276-315, 306-355 (5'-3', sense)

309-270, 354-315, 394-355, 571-532 (5'-3', antisense)

° Genotype IV/2b (Consensus Sequence of Figure 6E)

6-45, 135-174, 177-216, 309-348, 337-376, 375-414, 501-540
(5'-3', sense)

84-45, 213-174, 255-216, 387-348, 415-376, 453-414, 571-
532, 573-540 (5'-3', antisense)

5

Genotype 2c (SEQ ID NO:134)

194-233, 273-312, 279-318, 417-456, 423-462, 504-543, 505-
544, 517-556 (5'-3', sense)

272-233, 351-312, 354-315, 357-318, 450-411, 495-456, 501-
10 462, 573-543, 556-573 (5'-3', antisense)

Genotype 3 or Genotype V/3a (Consensus Sequence of Figure 6G)

8-47, 45-84, 68-107, 87-126, 88-127, 90-129, 111-150, 142-
15 181, 173-212, 177-216, 261-300,

276-315, 452-491, 520-559, 521-560, 529-568, 532-571, 533-
572. (5'-3', sense)

86-47, 123-84, 146-107, 165-126, 186-147, 189-150, 219-180,
250-211, 251-212, 255-216,

20 339-300, 530-491, 573-543, 573-557, 573-559, 573-560. (5'-
3', antisense)

Genotype 4 (Consensus Sequence of Figure 6H)

20-59 (5'-3', sense)

25 97-58, 98-59 (5'-3', antisense)

Genotype 4a (SEQ ID NO:139)

111-150, 150-189, 174-213, 183-222, 192-231, 261-300, 376-
415, 396-435, 531-570 (5'-3', sense)

30 186-147, 252-213, 270 -231, 339-300, 454-415 (5'-3',
antisense)

Genotype 4b (SEQ ID NO:141)

27-66, 30-69, 106-145, 271-310, 433-472, 447-486, 453-492
35 (5'-3', sense)

- ° 105-66, 183-144, 184-145, 345-306, 348-309, 349-310, 468-429, 510-471, 522-483, 570-531 (5'-3', antisense)

Genotype 4c (SEQ ID NO:143)

- 174-213, 180-219, 207-246, 231-270 (5'-3', sense)
5 249-210, 252-213, 258-219, 309-270, 504-465 (5'-3', antisense)

Genotype 4d (SEQ ID NO:145)

- 173-212, 188-327, 430-469 (5'-3', sense)
10 248-209, 249-210, 250-211, 251-212, 366-327, 508-469 (5'-3', antisense)

Genotype 4e (SEQ ID NO:142)

- 160-199, 267-306, 287-326, 288-327, 524-564 (5'-3', sense)
15 238-199, 345-306, 365-326, 216-177, 522-483 (5'-3', antisense)

Genotype 4f (SEQ ID NO:140)

- 18-57, 36-75, 228-267, 396-435 (5'-3', sense)
20 96-57, 114-75, 306-267 (5'-3', antisense)

Genotype 5 or 5a (Consensus Sequence of Figure 6I)

- 176-215, 177-216, 181-220, 195-234, 221-260, 252-291, 255-294, 396-435, 435-474, 447-486, 498-537 (5'-3', sense)
25 254-215, 299-260, 310-271, 330-291, 333-294, 354-315, 464-425, 471-432, 483-444, 570-531 (5'-3', antisense)

Genotype 6 or 6a (SEQ ID NO:154)

- 20-59, 136-175, 156-195, 159-198, 175-214, 185-224, 277-316, 278-317, 312-351, 348-387, 405-444, 406-445, 407-446, 408-447, 411-450, 432-471, 433-472, 435-474, 522-561 (5'-3', sense).
30 98-59, 214-175, 234-195, 237-198, 253-214, 262-223, 263-224, 354-315, 355-316, 382-343, 390-351, 426-387, 468-429, 483-444, 484-445, 485-446, 486-447, 489-450, 510-471, 511-
35

° 472, 513-474 (5'-3', antisense)

Such nucleotide domains may range from about 15 to about 100 bases in length with a more preferred range being about 30 to about 60 bases in length.

In an alternative embodiment, universal primers
5 able to hybridize to the nucleotide sequences of the core gene of HCV isolates belonging to all of the genotypes disclosed herein may be deduced from universally conserved nucleotide domains of the consensus sequence shown in Figures 6J and 6K. Examples of such nucleotide domains
10 include, but are not limited to, those shown below:

nucleotides 1-20, 1-25, 1-26, 1-27, 1-33, 50-89,
51-90, 52-91, 53-92, 61-100, 62-101, 77-116, 78-117, 79-
118, 80-119, 81-120, 82-121, 83-122, 84-123, 85-124, 86-
125, 97-136, 98-137, 99-138, 100-139, 101-140, 102-141,
15 329-368, 330-369, 331-370, 332-371, 354-393, 355-394, 356-395,
362-401, 363-402, 364-403, 365-404, 369-408, 442-481,
443-482, 457-496, 458-497, 475-514, 476-515, 477-516 (5'-3, sense); and

nucleotides 40-1, 41-2, 42-3, 43-4, 51-12, 52-13,
20 55-16, 56-17, 57-18, 58-19, 61-22, 62-23, 63-24,
64-25, 70-31, 124-85, 125-86, 126-87, 127-88, 128-89, 129-90,
136-97, 137-98, 138-99,
149-110, 150-111, 151-112, 152-113, 153-114, 154-115, 155-116,
156-117, 157-118, 158-119, 159-120, 170-131, 171-132,
25 172-133, 173-134, 174-135, 175-136, 403-364, 405-365, 406-366,
406-367, 430-391, 431-392, 432-393, 436-397, 437-398,
438-399, 439-400, 517-478, 518-479, 519-480, 532-493, 533-494,
550-511, 551-512 (5'-3', antisense)

Those skilled in the art would readily understand
30 that the term "antisense" as used herein refers to primer sequences which are the complementary sequence of the indicated consensus sequence or SEQ ID NO:. Further, provided with the above examples of regions of the consensus sequences or indicated SEQ ID NOS: from which to
35 deduce universal and genotype-specific primers, those

- ° skilled in the art would readily be able to select pairs of primers, one sense and one antisense, which would be useful in the detection of HCV genotypes via the PCR methods described herein.

In yet another embodiment, the sequences shown in SEQ ID NO.:103-154 and the resultant consensus sequences produced by alignment of these SEQ ID NOs as shown in Figures 6A-6K may also be useful in the design of hybridization probes specific for a given HCV genotype. Examples of nucleotide domains of the consensus sequence or SEQ ID NO of a given genotype from which genotype-specific hybridization probes may be deduced include, but are not limited to, those shown below where the sequence from which the domains are found is indicated in parentheses to the right of each genotype.

	<u>Genotype</u>	<u>Position</u>
15	1a (Consensus sequence of Figure 6A)	50-85 155-205 207-277 281-333 429-477 530-573
20	1b (Consensus sequence of Figure 6B)	81-131 159-225 252-318 411-472 530-573
25	2a (Consensus sequence of Figure 6D)	35-75 200-276 290-340 330-380 410-472 530-573
30	2b (Consensus sequence of Figure 6E)	20-70 149-199 191-241 240-285 261-318 323-373 351-401 389-439 429-477

35

0		530-573
	2c (SEQ ID NO:134)	208-258 230-276 290-345 411-460 430-490 530-573
5	3a (Consensus sequence of Figure 6G)	1-50 40-100 100-160 145-190 190-240 275-325 411-455 466-516 530-573
10		
	4a (SEQ ID NO:139)	35-85 145-195 200-250 255-305 341-390 390-440 530-573
15		
	4b (SEQ ID NO:141)	35-85 120-170 180-225 230-275 285-335 405-455 462-492 530-573
20		
	4c (SEQ ID NO:143)	35-85 190-246 245-295 282-318 372-415 440-480 530-573
25		
	4d (SEQ ID NO:145)	35-85 187-237 302-352 405-455 444-494 530-573
30		
	4e (SEQ ID NO:142)	35-85 57-84
35		

°		174-224 230-275 290-340 422-472 530-573
	4f (SEQ ID NO:140)	35-85 174-224
5		242-292 290-340 422-472 530-573
	5a (Consensus sequence of Figure 6I)	180-234 265-315 315-355 420-486 530-573
10		
	6a (SEQ ID NO:154)	34-84 150-200 180-230 230-290
15		291-333 341-395 429-490 530-573
	1 (Consensus sequence of Figure 6C)	192-241 435-495
20	2 (Consensus sequence of Figure 6F)	186-240 320-360 440-475
	4 (Consensus sequence of Figure 6H)	40-80

25 In yet another embodiment, universal hybridization probes may be derived from the consensus sequences shown in Figures 6J and 6K. Examples of nucleotide domains of the consensus sequences shown in Figure 6J and 6K from which universal hybridization probes may be derived include, but are not limited to, 1-33; 85-141; 364-408; 478-516.

30 The oligonucleotides of this invention can be synthesized using any of the known methods of oligonucleotide synthesis (e.g., the phosphodiester method of Agarwal et al. 1972, Agnew. Chem. Int. Ed. Engl. 11:451,

35

° the phosphotriester method of Hsiung et al. 1979, Nucleic
Acids Res 6:1371, or the automated diethylphosphoramidite
method of Baeu cage et al. 1981, Tetrahedron Letters
22:1859-1862), or they can be isolated fragments of
naturally occurring or cloned DNA. In addition, those
5 skilled in the art would be aware that oligonucleotides can
be synthesized by automated instruments sold by a variety
of manufacturers or can be commercially custom ordered and
prepared. In a preferred embodiment, the oligonucleotides
of the present invention are synthetic oligonucleotides.
10 The oligonucleotides of the present invention may range
from about 15 to about 100 nucleotides; with the preferred
sizes being about 20 to about 60 nucleotides; a more
preferred size being about 25 to about 50 nucleotides; and
a most preferred size being about 30 to about 40
15 nucleotides.

The present invention also relates to methods for
detecting the presence of HCV in a mammal, said methods
comprising analyzing the RNA of a mammal for the presence
of hepatitis C virus.

20 The RNA to be analyzed can be isolated from
serum, liver, saliva, lymphocytes or other mononuclear
cells as viral RNA, whole cell RNA or as poly(A)⁺ RNA.
Whole cell RNA can be isolated by methods known to those
skilled in the art. Such methods include extraction of RNA
25 by differential precipitation (Birnbiom, H.C. (1988)
Nucleic Acids Res., 16:1487-1497), extraction of RNA by
organic solvents (Chomczynski, P. et al. (1987) Anal.
Biochem., 162:156-159) and extraction of RNA with strong
denaturants (Chirgwin, J.M. et al. (1979) Biochemistry,
30 18:5294-5299). Poly(A)⁺ RNA can be selected from whole cell
RNA by affinity chromatography on oligo-d(T) columns (Aviv,
H. et al. (1972) Proc. Natl. Acad. Sci., 69:1408-1412). A
preferred method of isolating RNA is extraction of viral
RNA by the guanidinium-phenol-chloroform method of Bukh et
al. (1992a).
35

° The methods for analyzing the RNA for the presence of HCV include Northern blotting (Alwine, J.C. et al. (1977) Proc. Natl. Acad. Sci., 74:5350-5354), dot and slot hybridization (Kafatos, F.C. et al. (1979) Nucleic Acids Res., 7:1541-1522), filter hybridization (Hollander, M.C. et al. (1990) Biotechniques; 9:174-179), RNase protection (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY) and reverse-transcription polymerase chain reaction (RT-PCR) (Watson, J.D. et al. (1992) in "Recombinant DNA" Second Edition, W.H. Freeman and Company, New York).

A preferred method for analyzing the RNA is RT-PCR. In this method, the RNA can be reverse transcribed to first strand cDNA using a primer or primers derived from the nucleotide sequences shown in SEQ ID NOS:1-51 or SEQ ID NOS:103-154 or sequences complementary to those described. Once the cDNAs are synthesized, PCR amplification is carried out using pairs of primers designed to hybridize with sequences in the HCV E1 or core cDNA which are an appropriate distance apart (at least about 50 nucleotides) to permit amplification of the cDNA and subsequent detection of the amplification product. Alternatively, one can amplify both E1 and core cDNA sequences by using a primer pair where one primer hybridizes with the E1 cDNA sequence and the other primer hybridizes with the core cDNA sequence. Each primer of a pair is a single-stranded oligonucleotide of about 20 to about 60 bases in length with a more preferred range being about 30 to about 50 bases in length where one primer (the "upstream" primer) is complementary to the original RNA and the second primer (the "downstream" primer) is complementary to the first strand of cDNA generated by reverse transcription of the RNA. The target sequence is generally about 100 to about 300 base pairs long but can be as large as 500-1500 base pairs. Optimization of the amplification reaction to

- ° obtain sufficiently specific hybridization to the nucleotide sequence of interest (either E1 or core or both E1 and core) is well within the skill in the art and is preferably achieved by adjusting the annealing temperature.

In one embodiment, the primer pairs selected to amplify E1 and core cDNAs are universal primers. By "universal", as used to describe primers throughout the claims and specification, is meant those primer pairs which can amplify E1 and/or core gene fragments derived from an HCV isolate belonging to any one of the genotypes of HCV described herein. Purified and isolated universal primers for E1 cDNAs are used in Example 1 of the present invention and are shown as SEQ ID NOS:207-212 where SEQ ID NOS:207 and 208 represent one pair of primers, SEQ ID NOS:209 and 210 represent a second pair of primers and SEQ ID NOS:211-212 represent a third pair of primers. Nucleotide domains of the consensus sequence shown in Figure 6J from which universal primers for core cDNAs may be deduced have previously been disclosed within the present specification. Alternatively, a universal primer for E1 cDNA sequence and a universal primer for core cDNA sequence may be used as a universal primer pair to amplify both E1 and core cDNAs.

In an alternative embodiment, primer pairs selected to amplify E1 and/or core cDNAs are genotype-specific primers. In the present invention, genotype-specific primer pairs can readily be derived from the following genotype-specific E1 nucleotide domains: nucleotides 197-238 and 450-480 of the consensus sequence of genotype I/1a shown in Figure 1A; nucleotides 197-238 and 450-480 of the consensus sequence of genotype II/1b shown in Figure 1B; nucleotides 199-238 and 438-480 of the consensus sequence of genotype III/2a shown in Figure C; nucleotides 124-177 and 450-480 of the consensus sequence of genotype IV/2b shown in Figure 1D; nucleotides 124-177, 193-238 and 436-480 of SEQ ID NO:34 (genotype 2C); nucleotides 168-207, 294-339 and 406-480 of the consensus

° sequence of genotype V/3a shown in Figure 1E; nucleotides 145-183 and 439-480 of SEQ ID NO:40 (genotype 4a); nucleotides 168-207 and 432-480 of SEQ ID NO:41 (genotype 4b); nucleotides 130-183 and 450-480 of the consensus sequence of genotype 4c shown in Figure 1F; nucleotides 130-183 and 450-480 of SEQ ID NO:44 (genotype 4d); nucleotides 166-208 and 437-480 of the consensus sequence of genotype 5a shown in Figure 1b and nucleotides 168-207, 216-252 and 429-480 of SEQ ID NO:51 (genotype 6a). Genotype-specific HCV core nucleotide domains from which genotype-specific primers may be deduced have previously been described herein. Those skilled in the art would readily appreciate that in a pair of genotype-specific primers, each primer is derived from different nucleotide domains specific for a given genotype. Also, it is understood by those skilled in the art that each pair of primers comprises one primer which is complementary to the original viral RNA and the other which is complementary to the first strand of cDNA generated by reverse transcription of the viral RNA. For example, in a pair of genotype-specific primers for genotype 4b, one primer would have a nucleotide sequence derived from region 168-207 of SEQ ID NO:40 and the other primer would have a nucleotide sequence which is the complement of region 432-480 of SEQ ID NO:40. One skilled in the art would readily recognize that such genotype-specific domains would also be useful in designing oligonucleotides for use as genotype-specific hybridization probes. Indeed, genotype-specific hybridization probes deduced from the E1 and core sequences of the present invention have been previously disclosed herein.

The amplification products of PCR can be detected either directly or indirectly. In one embodiment, direct detection of the amplification products is carried out via labelling of primer pairs. Labels suitable for labelling the primers of the present invention are known to one skilled in the art and include radioactive labels, biotin,

avidin, enzymes and fluorescent molecules. The derived labels can be incorporated into the primers prior to performing the amplification reaction. A preferred labelling procedure utilizes radiolabeled ATP and T4 polynucleotide kinase (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, NY). Alternatively, the desired label can be incorporated into the primer extension products during the amplification reaction in the form of one or more labelled dNTPs. In the present invention, the labelled amplified PCR products can be detected by agarose gel electrophoresis followed by ethidium bromide staining and visualization under ultraviolet light or via direct sequencing of the PCR-products. Thus, in one embodiment, the present invention relates to a method for determining the genotype of a hepatitis C virus present in a mammal where said method comprises: amplifying RNA of a mammal via RT-PCR using labelled genotype-specific primers for the amplification step of the cDNA produced by reverse transcription.

In yet another embodiment, unlabelled amplification products can be detected via hybridization with labelled nucleic acid probes radioactively labelled or, labelled with biotin, in methods known to one skilled in the art such as dot and slot blot hybridization (Kafatos, F.C. et al. (1979) or filter hybridization (Hollander, M.C. et al. (1990)).

In one embodiment, the nucleic acid sequences used as probes are selected from, and substantially homologous to, SEQ ID NOs:1-51 and/or SEQ ID NOs:103-154. Such probes are useful as universal probes in that they can detect PCR-amplification products of E1 and/or core cDNAs of an HCV isolate belonging to any of the HCV genotypes disclosed herein. The size of these probes can range from about 200 to about 500 nucleotides. In an alternative embodiment, the sequence alignments shown in Figures 1A-1H

° and 6A-6J may be used to design oligonucleotides useful as universal hybridization probes. Examples of core and envelope nucleotide domains from which such universal oligonucleotides may be deduced are disclosed herein.

In yet another embodiment, the present invention relates to a method for determining the genotype of a hepatitis C virus present in a mammal where said method comprises:

- (a) amplifying RNA of a mammal via RT-PCR to produce amplification products;
- 10 (b) contacting said products with at least one genotype-specific oligonucleotide; and
- (c) detecting complexes of said products which bind to said oligonucleotide(s).

In this method, one embodiment of said amplification step is carried out using the universal primers for E1 or core cDNAs as disclosed above. In step (b) of this method, the genotype-specific sequences used as probes may be deduced from the genotype-specific E1 and core nucleotide domains disclosed herein. These probes are useful in specifically detecting PCR-amplification products of E1 or core cDNAs of HCV isolates belonging to one of the HCV genotypes disclosed herein. In a preferred embodiment, these probes are used alone or in combination with other probes specific to the same genotype.

For example, a probe having a sequence according to SEQ ID NO:213 can be used alone or in combination with a probe having a sequence according to SEQ ID NO:214. The probes used in this method can range in size from about 15 to about 100 nucleotides with a more preferred range being about 30 to about 70 nucleotides. Such probes can be synthesized as described earlier.

In an alternative embodiment, the genotype of the amplification product of step (a) may be determined by using the nucleic acid sequences shown in SEQ ID NOS: 1-51 and 103-154 as probes (Delwart, E. et al. (1993)) Science,

° 262: 1257-1261). Probes utilized in the method of Delwart et al. may range in size from about 100 to about 1,000 nucleotides with a more preferred probe size being about 200 to about 800 base pairs and a most preferred probe size being about 300 to about 700 nucleotides.

5 The nucleic acid sequence used as a probe to detect PCR amplification products of the present invention can be labeled in single-stranded or double-stranded form. Labelling of the nucleic acid sequence can be carried out by techniques known to one skilled in the art. Such
10 labelling techniques can include radiolabels and enzymes (Sambrook, J. et al. (1989) in "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Press, Plainview, New York). In addition, there are known non-radioactive techniques for signal amplification including methods for
15 attaching chemical moieties to pyrimidine and purine rings (Dale, R.N.K. et al. (1973) Proc. Natl. Acad. Sci., 70:2238-2242; Heck, R.F. (1968) S. Am. Chem. Soc., 90:5518-5523), methods which allow detection by chemiluminescence (Barton, S.K. et al. (1992) J. Am. Chem. Soc., 114:8736-
20 8740) and methods utilizing biotinylated nucleic acid probes (Johnson, T.K. et al. (1983) Anal. Biochem., 133:126-131; Erickson, P.F. et al. (1982) J. of Immunology Methods, 51:241-249; Matthaiei, F.S. et al. (1986) Anal. Biochem., 157:123-128) and methods which allow detection by
25 fluorescence using commercially available products.

The present invention also relates to computer analysis of the amino acid sequences shown in SEQ ID NOS:52-102 by the program GENALIGN. This analysis groups the 51 amino acid sequences shown in SEQ ID NOS:52-102 into
30 twelve genotypes based upon the degree of variation of the amino acid sequences. For the purposes of the present invention, the amino acid sequence identity of E1 amino acid sequences of the same genotype ranges from about 85% to about 100% whereas the identity of E1 amino acid
35 sequences of different genotypes ranges from about 45% to

° about 80%.

The grouping of SEQ ID NOs:52-102 into twelve HCV genotypes is shown below:

	<u>SEQ ID NOs:</u>	<u>Genotypes</u>
5	52-59	I/1a
	60-76	II/1b
	77-80	III/2a
	81-84	IV/2b
	85	2c
	86-90	V/3a
	91	4a
10	92	4b
	93-94	4c
	95	4d
	96-101	5a
	102	6a

For those genotypes containing more than one E1 amino acid sequence, computer alignment of the constituent sequences of each genotype was conducted using the computer program GENALIGN in order to produce a consensus sequence for each genotype. These alignments and their resultant consensus sequences are shown in Figures 2A-G for the seven genotypes (I/1a, II/1b, III/2a, IV/2b, V/3a, 4c and 5a) which comprise more than one sequence. Further alignment of the consensus sequences shown in Figures 2A-G with the amino acid sequences of SEQ ID NO:85 (genotype 2c); SEQ ID NO:91 (genotype 4a); SEQ ID NO:92 (genotype 4b); SEQ ID NO:95 (genotype 4d) and SEQ ID NO:102 (genotype 6a) to produce a consensus amino acid sequence for all twelve genotypes is shown in Figure 2H. The multiple alignment of E1 amino acid sequences shown in Figures 2A-H produces consensus sequences which serve to highlight regions of homology and non-homology between E1 amino acid sequences of the same genotype and of different genotypes and hence, these alignments can readily be used by those skilled in the art to design peptides useful in assays and vaccines for the diagnosis and prevention of HCV infection.

In another embodiment, the computer analysis of

- ° SEQ ID NOS: 155-206 by the probe genome results in distribution of the 52 HCV core sequences into 14 genotypes based upon identification of genotype-specific amino acid sequences.

5 The grouping of SEQ ID NOS: 155-206 into 14 HCV genotypes is shown below:

	<u>SEQ ID NOS:</u>	<u>Genotypes</u>
	155-160	I/1a
	161-176	II/1b
	177-180	III/2a
10	181-185	IV/2b
	186	2c
	187-190	V/3a
	191	4a
	193	4b
	195	4c
	196	4c
15	197	4d
	194	4e
	192	4f
	198-205	5a
	206	6a

20 These fourteen genotypes can be further grouped into six major genotypes designated genotypes 1-6 as described earlier for the core nucleotide sequences of the present application. Computer alignment of the amino acid sequences disclosed in SEQ ID NOS: 155-206 are shown in figures 7A-7J. As with the multiple alignments of the E-1

25 amino acid sequences, the consensus sequences shown in figure 7A-7J serve to highlight regions of homology and nonhomology between core amino acid sequences of the same genotype and of different genotypes and hence, these alignments can readily be used by those skilled in the art to design peptides useful in assays and vaccines for the

30 diagnosis and prevention of HCV infection.

Examples of purified and isolated peptides deduced from the alignments shown in Figures 2A-2H include, but are not limited to, SEQ ID NOS:240-263 wherein these peptides are derived from two regions of the amino acid

35

° sequences shown in Figures 2A-H, amino acids 48-80 and amino acids 138-160. The peptides shown in SEQ ID NOS. 240-263 are useful as genotype-specific diagnostic reagents since they are capable of detecting an immune response specific to HCV isolates belonging to a single genotype.

5 The genotype-specificity of the peptides shown in SEQ ID NOS:240-263 are as follows: SEQ ID NOS:240 and 252 are specific for genotype IV/2b; SEQ ID NOS:241 and 253 are specific for genotype 2c; SEQ ID NOS:242 and 254 are specific for genotype III/2a; SEQ ID NOS:243 and 255 are

10 specific for genotype V/a; SEQ ID NOS:244 and 256 are specific for genotype II/1b; SEQ ID NOS:245 and 257 are specific for genotype I/1a; SEQ ID NOS:246 and 258 are specific for genotype 4a; SEQ ID NOS:247 and 259 are specific for genotype 4c; SEQ ID NOS:248 and 260 are

15 specific for genotype 4d; SEQ ID NOS:249 and 261 are specific for genotype 4b; SEQ ID NOS:250 and 262 are specific for genotype 5a and SEQ ID NOS:251 and 263 are specific for genotype 6a. In SEQ ID NO:240, Xaa at position 22 is a residue of Ala or Thr, Xaa at position 24

20 is a residue of Val or Ile, Xaa at position 26 is a residue of Val or Met; in SEQ ID NO:242, Xaa at position 5 is a Ser or Thr residue, Xaa at position 11 is an Arg or Gln residue, Xaa at position 12 is an Arg or Gln residue; in

25 SEQ ID NO:243, Xaa at position 3 is a Pro or Ser residue, Xaa at position 33 is a Leu or Met residue; in SEQ ID NO:244, Xaa at position 5 is a Thr or Ala residue, Xaa at position 13 is a Gly, Ala, Ser, Val or Thr residue, Xaa at position 14 is a Ser, Thr or Asn residue, Xaa at position 15 is a Val or Ile residue, Xaa at position 16 is a Pro or

30 Ser residue, Xaa at position 18 is a Thr or Lys residue, Xaa at position 19 is a Thr or Ala residue, Xaa at position 22 is an Arg or His residue, Xaa at position 32 is an Ala, Val or Thr residue; in SEQ ID NO:245, Xaa at position 3 is an Ala or Pro residue, Xaa at position 4 is a Val or Met residue, Xaa at position 5 is a Thr or Ala residue, Xaa at

35

° position 17 is a Thr or Ala residue, Xaa at position 18 is a Thr or Ala residue, Xaa at position 23 is a His or Tyr residue; in SEQ ID NO:247, Xaa at position 10 is a Val or Ala residue, Xaa at position 11 is a Ser or Pro residue, Xaa at position 18 is an Asp or Glu residue Xaa at position 20 is a Leu or Ile residue; in SEQ ID NO:250, Xaa at position 3 is a Gln or His residue, Xaa at position 12 is an Asn, Ser or Thr residue, Xaa at position 13 is a Leu or Phe residue, Xaa at position 23 is an Ala or Val residue; in SEQ ID NO:252, Xaa at position 16 is a Val or Ala residue, Xaa at position 18 is a Glu or Gln residue; in SEQ ID NO:254, Xaa at position 2 is an Ala or Thr residue, Xaa at position 4 is a Met or Leu residue, Xaa at position 9 is an Ala or Val residue, Xaa at position 17 is an Ile or Leu residue, Xaa at position 20 is an Ile or Val residue, Xaa at position 21 is a Ser or Gly residue; in SEQ ID NO:151, Xaa at position 9 is a Val or Ile residue, Xaa at position 16 is a Leu or Val residue, Xaa at position 20 is an Ile or Leu residue; in SEQ ID NO:256, Xaa at position 2 is an Ala or Thr residue, Xaa at position 6 is a Val or Leu residue, Xaa at position 12 is an Ile or Leu residue, Xaa at position 16 is a Val or Ile residue, Xaa at position 17 is a Val, Leu or Met residue, Xaa at position 19 is a Met or Val residue, Xaa at position 21 is an Ala or Thr residue; in SEQ ID NO:257, Xaa at position 2 is a Thr or Ala residue, Xaa at position 6 is a Val, Ile or Met residue, Xaa at position 12 is an Ile or Val residue, Xaa at position 16 is a Ile or Val residue; in SEQ ID NO:155, Xaa at position 5 is a Leu or Val residue, Xaa at position 21 is a Thr or Ala residue; in SEQ ID NO:262, Xaa at position 1 is a Thr or Ala residue, Xaa at position 5 is a Val or Leu residue, Xaa at position 9 is a Leu, Met or Val residue, Xaa at position 23 is a Gly or Ala residue.

Examples of core amino acid domains from which genotype-specific peptides may be deduced, include but are not limited to, those shown below where the sequence in

- ° which the indicated domains are found is given in parentheses to the right of each genotype:

	<u>Genotype</u>	<u>Amino Acid Domains</u>
	1a (consensus sequence of Figure 7A)	67-78
	1b (consensus sequence of Figure 7B)	67-78
5	2 (consensus sequence of Figure 7F)	66-81
		110-119
	2a (consensus sequence of Figure 7D)	67-78
		115-125
	2b (consensus sequence of Figure 7E)	67-78
		123-133
	2c (SEQ ID NO:186)	67-78
		75-81
10	3a (consensus sequence of Figure 7G)	184-191
		8-22
		32-46
		67-78
		158-170
		180-191
	4 (consensus sequence of Figure 7H)	14-23
	4a (SEQ ID NO:191)	67-78
15	4b (SEQ ID NO:193)	45-57
		67-78
	4c (SEQ ID NO:195)	67-78
	4d (SEQ ID NO:197)	67-78
	4e (SEQ ID NO:194)	67-78
	4f (SEQ ID NO:192)	67-78
	5a (consensus sequence of Figure 7J)	67-78
20	6a (SEQ ID NO:206)	67-78
		101-108
		144-155
		157-163

- Those skilled in the art would be aware that the peptides of the present invention or analogs thereof can be synthesized by automated instruments sold by a variety of manufacturers or can be commercially custom-ordered and prepared. The term analog has been described earlier in the specification and for purposes of describing the peptides of the present invention, analogs can further include branched, cyclic or other non-linear arrangements of the peptide sequences of the present invention.

- Alternatively, peptides can be expressed from nucleic acid sequences where such sequences can be DNA, cDNA, RNA or any variant thereof which is capable of

° directing protein synthesis. In one embodiment, restriction digest fragments containing a coding sequence for a peptide can be inserted into a suitable expression vector that functions in prokaryotic or eukaryotic cells. Such restriction digest fragments may be obtained from clones isolated from prokaryotic or eukaryotic sources which encode the peptide sequence.

Suitable expression vectors and methods of isolating clones encoding the peptide sequences of the present invention have previously been described. In yet another embodiment, an oligonucleotide capable of directing host organism synthesis of the given peptide may be synthesized and inserted into the expression vector.

The preferred size of the peptides of the present invention is from about 8 to about 100 amino acids in length when the peptides are chemically synthesized with a more preferred size being about 8 to about 30 amino acids and a most preferred size being about 10 to about 20 amino acids in length. For recombinantly expressed peptides, the size may range from about 20 to about 190 amino acids in length with a more preferred size being about 70 amino acids.

The present invention further relates to the use of genotype-specific peptides in methods of detecting antibodies against a specific genotype of HCV in biological samples. In one embodiment, at least one genotype-specific peptide deduced from a genotype-specific core or E1 amino acid domain may be used in any of immunoassays described herein to detect antibodies specific for a single genotype of HCV. In another embodiment, at least one genotype-specific peptide deduced from a genotype-specific core nucleotide domain and at least one genotype-specific peptide deduced from an E1 amino acid domain may be used in an immunoassay to detect antibodies against a single genotype of HCV. A preferred immunoassay is ELISA.

It is understood by those skilled in the art that

° the diagnostic assays described herein using genotype-specific oligonucleotides or genotype-specific peptides can be useful in assisting one skilled in the art to choose a course of therapy for the HCV-infected individual.

In an alternative embodiment, a mixture of
5 genotype-specific peptides can be used in an immunoassay to detect antibodies against multiple genotypes of HCV disclosed herein. For example, a mixture of genotype-specific peptides deduced from E1 amino acid sequences may comprise at least one peptide selected from SEQ ID NOS:244-
10 245 and 256-257; one peptide selected from SEQ ID NOS:240, 242, 252 and 254; one peptide selected from SEQ ID NOS:246-249 and 258-261; one peptide selected from SEQ ID NOS:250 and 262; one peptide selected from SEQ ID NOS:243 and 255; one peptide selected from SEQ ID NOS:242 and 254 and one
15 peptide selected from SEQ ID NOS:244 and 263. In a preferred embodiment, the peptides of the present invention can be used in an ELISA assay as described previously for recombinant E1 and core proteins.

In an alternative embodiment, the peptide(s)
20 utilized in an immunoassay to detect all the genotypes of HCV disclosed herein may be a universal peptide deduced from universally conserved amino acid domains of the E1 or core proteins disclosed herein.

Examples of universally conserved core amino acid
25 domains within the consensus sequence shown in Figure 7J from which universal peptides may be deduced include, but are not limited to amino acid domains 23-35, 53-66, 93-108, 122-138, 150-156, and 165-181 of the consensus sequence. Examples of universally conserved E1 amino acid domains
30 within the HCV E1 protein are located within the consensus sequence for the 51 HCV E1 proteins shown in Figure 2H of the present application. Examples of universally conserved domains within the consensus sequence shown in Figure 2H include, but are not limited to, amino acid domains 10-20,
35 111-120, and 124-137 of the consensus sequence. The

° universal peptides of the present invention may be used in an immunoassay to detect antibodies in patient sera specific for any of the genotypes of HCV disclosed herein.

The peptides of the present invention or analogs thereof may be prepared in the form of a kit, alone or in combinations with other reagents such as secondary antibodies, for use in immunoassay.

In another embodiment, the genotype-specific and universal peptides of the present invention may be used to produce antibodies that will react against HCV E1 or core proteins in immunoassays. In one embodiment, a genotype-specific E1 or core peptide can be used alone or in combination with other E1 or core peptides specific to the same genotype as immunogens to produce antibodies specific to HCV proteins of a single genotype.

In another embodiment, a mixture of peptides specific for different genotypes may be used to produce antibodies that will react with HCV proteins of any genotype disclosed herein. More preferably, antibodies reactive with HCV proteins of any genotype may be produced by immunizing an animal with universal peptide(s) of the present invention. Examples of immunoassays in which such antibodies could be utilized to detect HCV E1 and core proteins in biological samples include, but are not limited to, radioimmunoassays and ELISAs. Examples of biological samples in which HCV E1 and core proteins could be detected includes, but it is not limited to, serum, saliva and liver.

Of course, those skilled in the art would readily understand that the genotype-specific and universal peptides of the present invention and expression vectors containing nucleic acid sequence capable of directing host organism synthesis of these peptides could also be used as vaccines against hepatitis C. Formulations suitable for administering the peptide(s) and expression vectors of the present invention as immunogen, routes of administration,

- ° pharmaceutical compositions comprising the peptides expression vectors and so forth are the same as those previously described for recombinant E1 and core proteins.

The genotype-specific and universal peptides of the present invention and expression vectors containing nucleic acid sequence capable of direct host organism synthesis of these peptides may also be supplied in the form of a kit, alone, or in the form of a pharmaceutical composition as described above for recombinant E1 and core proteins.

Any articles or patents referenced herein are incorporated by reference. The following examples illustrate various aspects of the invention but are in no way intended to limit the scope thereof.

15

20

25

30

35

MATERIALS

Serum used in these examples was obtained from 84 anti-HCV positive individuals who were previously found to be positive for HCV RNA in a cDNA PCR assay with primer set a from the 5' NC region of the HCV genome (Bukh, J. et al. (1992 (b)) Proc. Natl. Acad. Sci. USA 89:4942-4946). These samples were from 12 countries: Denmark (DK); Dominican Republic (DR); Germany (D); Hong Kong (HK); India (IND); Sardinia, Italy (S); Peru (P); South Africa (SA); Sweden (SW); Taiwan (T); United States (US); and Zaire (Z).

Example 1

Identification of the cDNA Sequence
of the E1 Gene of 51 Isolates of HCV via
RT-PCR Analysis of Viral RNA Using Universal Primers

Viral RNA was extracted from 100 µl of serum by the guanidinium-phenol-chloroform method and the final RNA solution was divided into 10 equal aliquots and stored at -80°C as described (Bukh, et al. (1992 (a))). The sequences of the synthetic oligonucleotides used in the RT-PCR assay, deduced from the sequence of HCV strain H-77 (Ogata, N. et al. (1991) Proc. Natl. Acad. Sci. USA 88:3392-3396), are shown as SEQ ID NOs:207-212. One aliquot of the final RNA solution, equivalent to 10 µl of serum, was used for cDNA synthesis that was performed in a 20 µl reaction mixture using avian myeloblastosis virus reverse transcriptase (Promega, Madison, WI) and SEQ ID NO:208 as a primer. The resulting cDNA was amplified in a "nested" PCR assay by Taq DNA polymerase (Amplitaq, Perkin-Elmer/Cetus) as described previously (Bukh et al. (1992a)) with primer set e (SEQ ID NOs:207-210). Precautions were taken to avoid contamination with exogenous HCV nucleic acid (Bukh et al. 1992a)), and negative controls (normal, uninfected serum) were interspersed between every test sample in both the RNA extraction and cDNA PCR procedures. No false positive results were observed in the analysis. In most instances,

° amplified DNA (first or second PCR products) was reamplified with primers SEQ ID NO:211 and SEQ ID NO:212 prior to sequencing since these two primers contained EcoRI sites which would facilitate future cloning of the E1 gene. Amplified DNA was purified by gel electrophoresis followed
5 by glass-milk extraction (Geneclean, BIO 101, LaJolla, CA) and both strands were sequenced directly by the dideoxy-nucleotide chain termination method (Bachman, B. et al. (1990) Nucl. Acids Res. 18:1309) with phage T7 DNA polymerase (Sequenase, United States Biochemicals, 10 Cleveland, OH), [alpha ³⁵S]dATP (Amersham, Arlington Heights, IL) or [alpha ³³P] dATP (Amersham or DuPont, Wilmington, DE) and sequencing primers. RNA extracted from serum containing HCV strain H-77, previously sequenced by Ogata, N. et al. (1991), was amplified with primer set e
15 (SEQ ID NOS:207-210) and sequenced in parallel as a control. The nucleotide sequences of the envelope 1 (E1) gene of all 51 HCV isolates are shown as SEQ ID NOS:1 - 51. In all 51 HCV isolates, the E1 gene was exactly 576 nucleotides in length and did not have any in-frame stop
20 codons.

Example 2

Computer Analysis of the Nucleotide and Deduced Amino Acid Sequences of the E1 Gene of 51 HCV Isolates

25 Multiple computer-generated alignments of the nucleotide (SEQ ID NOS:1-51, Figures 1A-H) and deduced amino acid sequences (SEQ ID NOS:52-102, Figures 2A-H) of the cDNAs of the 51 HCV isolates constructed using the computer program GENALIGN (Miller, R.H. et al. (1990) Proc. Natl. Acad. Sci. USA 87:2057-2061) resulted in the 51 HCV
30 isolates being divided into twelve genotypes based upon the degree of variation of the E1 gene sequence as shown in table 1.

Table 1. Percent nucleotide (nt) and amino acid (aa) sequence identity of the EI gene among the 12 HCV genotypes.

	I/1a	II/1b	III/2a	IV/2b	2c	(V)/3a	4a	4b	4c	4d	5a	6a	nt:
aa:	89.9-97.6	72.0-76.2	59.2-63.7	56.1-58.3	60.8-62.8	63.0-66.3	63.9-67.2	64.9-66.8	62.7-64.4	67.7-69.4	62.3-67.2	62.2-63.9	I/1a
	88.9-97.9	88.9-97.9	58.3-62.2	53.8-57.5	60.1-61.5	63.9-67.2	60.9-63.7	63.4-65.8	61.6-65.1	63.0-65.5	62.2-66.5	61.6-63.0	II/1b
	91.1-98.4		88.0-91.3	69.1-71.0	72.7-73.6	58.0-60.8	61.5-62.7	58.9-60.4	59.7-63.4	58.7-61.3	56.6-60.8	55.0-56.8	III/2a
	75.5-80.7	90.1-97.9		92.7-95.0	67.5-68.9	56.3-58.3	58.9-60.8	56.4-57.6	57.1-59.9	57.5-59.0	53.5-56.6	53.6-55.2	IV/2b
	58.3-64.6	52.6-56.8	89.1-92.7		---	57.5-58.2	59.2	58.5	58.0-58.3	58.9	56.9-57.1	57.6	2c
	54.2-56.8	51.0-54.2	69.3-72.9	93.8-96.4		93.8-99.1	64.4-65.3	62.7-64.1	60.9-62.5	62.3-63.9	61.8-64.4	58.0-58.9	(V)/3a
	56.3-60.4	52.6-55.7	74.5-77.1	67.7-69.8	---		---	74.8	75.5-78.0	74.8	62.8-64.6	62.0	4a
	64.1-68.8	66.7-70.8	54.7-58.9	54.2-56.8	52.1-53.6	94.3-98.4		---	74.0-74.8	72.0	63.9-64.6	62.7	4b
	69.3-73.4	64.6-67.2	62.0-63.0	58.9-60.4	58.3	66.1-68.8	---		90.1	77.6-78.6	62.7-64.8	63.0-64.4	4c
	66.7-69.3	66.1-70.3	53.6-56.3	52.1-53.1	53.6	62.0-64.6	76.0	---	---	---	64.4-66.1	64.1	4d
	66.1-72.9	64.6-69.3	55.2-61.5	54.2-58.3	54.7-58.3	63.0-65.6	77.1-81.3	79.2-80.2	89.6		90.1-95.7	60.6-63.2	5a
	73.7-75.5	66.7-70.3	56.3-58.9	55.2-55.7	54.2	63.5-64.6	78.1	77.6	82.8	---	---	---	6a
	66.1-73.4	64.1-70.3	52.6-57.3	50.5-53.1	54.2-56.8	60.4-64.1	67.2-68.2	65.1-67.2	67.7-71.4	69.3-71.4	92.7-97.4		
	64.6-65.6	62.3-65.6	49.0-51.0	49.0-50.5	50.5	57.8-58.9	66.1	62.5	66.1-67.2	66.7	62.0-63.5	---	

Nucleotide sequences analyzed in compiling the above table are shown in SEQ ID NOs:1-51 while the amino acid sequences analyzed are shown in SEQ ID NOs:52-102. The grouping of SEQ ID NOs: into genotypes is previously described in the specification.

° The nucleotide and amino acid sequence identity of HCV isolates of the same genotype was in the range of 88.0-99.1% and 89.1-98.4%, respectively, whereas that of HCV isolates of different genotypes was in the range of 53.5-78.6% and 49.0-82.8%, respectively. The latter
5 differences are similar to those found when comparing the envelope gene sequences of the various serotypes of the related flaviviruses, as well as other RNA viruses. When microheterogeneity in a sequence was observed, defined as more than one prominent nucleotide at a specific position,
10 the nucleotide that was identical to that of the HCV prototype (HCV1, Choo et al. (1989)) was reported if possible. Alternatively, the nucleotide that was identical to the most closely related isolate is shown.

 Analysis of the consensus sequence of the E1
15 protein of the 51 HCV isolates from this study demonstrated that a total of 60 (30.3%) of the 192 amino acids of the E1 protein were invariant among these isolates (Fig. 3). Most impressive, all 8 cysteine residues as well as 6 of 8
20 proline residues were invariant. The most abundant amino acids (e.g. alanine, valine and leucine) showed a very low degree of conservation. The consensus sequence of the E1 protein contained 5 potential N-linked glycosylation sites. Three sites at positions 209, 305 and 325 were maintained in all 51 HCV isolates. A site at position 196 was
25 maintained in all isolates except the sole isolate of genotype 2c. Also, a site at position 234 was maintained in all isolates except one isolate of genotype I/1a, all four isolates of genotype IV/2b and the sole isolate of genotype 6a. Conversely, only genotype IV/2b isolates had
30 a potential glycosylation site at position 233. Further analysis revealed a highly conserved amino acid domain (aa 302-328) in the E1 protein with 20 (74.1%) of 27 amino acids invariant among all 51 HCV isolates. It is possible that the 5' and 3' ends of this domain are conserved due to
35 important cysteine residues and N-linked glycosylation

° sites. The central sequence, 5'-GHRMAWDM-3' (aa 315-323), may be conserved due to additional functional constraints on the protein structure. Finally, although the amino acid sequence surrounding the putative E1 protein cleavage site was variable, an amino acid doublet (GV) at position 380 was invariant among all HCV isolates.

A dendrogram of the genetic relatedness of the E1 protein of selected HCV isolates representing the 12 genotypes is shown in Fig. 4. This dendrogram was constructed using the program CLUSTAL (Higgins, D.G. et al. (1988) Gene, 73:237-244) and had a limit of 25 sequences. The scale showing percent identity was added based upon manual calculation. From the 51 HCV isolates for which the complete sequence of the E1 gene region was obtained, 25 isolates representing the twelve genotypes were selected for analysis. This dendrogram in combination with the analysis of the E1 gene sequence of 51 HCV isolates in Table 1 demonstrates extensive heterogeneity of this important gene.

The worldwide distribution of the 12 genotypes among 74 HCV isolates is depicted in Fig. 5. The complete E1 gene sequence was determined in 51 of these HCV isolates (SEQ ID NOs:1-51), including 8 isolates of genotype I/1a, 17 isolates of genotype II/1b and 26 isolates comprising genotypes III/2a, IV/2b, 2c, 3a, 4a-4d, 5a and 6a. In the remaining 23 isolates, all of genotypes I/1a and II/1b, the genotype assignment was based on a partial E1 gene sequence since they did not represent additional genotypes in any of the 12 countries. The number of isolates of a particular genotype is given in each of the 12 countries studied. Of the twelve genotypes, genotypes I/1a and II/1b were the most common accounting for 48 (65%) of the 74 isolates. Analysis of the E1 gene sequences available in the GenBank data base at the time of this study revealed that all 44 such sequences were of genotypes I/1a, II/1b, III/2a and IV/2b. Thus, based upon E1 gene analysis, 8 new genotypes

° of HCV have been identified.

Also of interest, different HCV genotypes were frequently found in the same country, with the highest number of genotypes (five) being detected in Denmark. Of the twelve genotypes, genotypes I/1a, II/1b, III/2a, IV/2b and V/3a were widely distributed with genotype II/1b being identified in 11 of 12 countries studied (Zaire was the only exception). In addition, while genotypes I/1a and II/1b were predominant in the Americas, Europe and Asia, several new genotypes were predominant in Africa.

It was also found that genotypes I/1a, II/1b, III/2a, IV/2b and V/3a of HCV were widely distributed around the world, whereas genotypes 2c, 4a, 4b, 4d, 5a and 6a were identified only in discreet geographical regions. For example, the majority of isolates in South Africa comprised a new genotype (5a) and all isolates in Zaire comprised 3 new closely related genotypes (4a, 4b, 4c). These genotypes were not identified outside Africa.

Example 3

Identification of the cDNA Sequence Of The Core Gene Of 52 Isolates Of HCV

Viral RNA extraction, cDNA synthesis and "nested" PCR were carried out as in Example 1. For the cDNA PCR assay HCV-specific synthetic oligonucleotides deduced from previously determined sequences that flank the C gene were used. Amplified DNA was purified by gel electrophoresis followed by glass-milk extraction as described in Example 1 or by electroelution and both strands were sequenced directly. In 44 of the 52 HCV isolates studied the procedures for direct sequencing described in Example 1 were utilized. For a number of the HCV isolates confirmatory sequencing was performed with the Applied Biosystems 373A automated DNA sequencer and 8 HCV isolates of genotype I/1a or II/1b were sequenced exclusively by this method. All 73 negative control samples interspersed

° among the test samples were negative for HCV RNA.

The amplified DNA fragment obtained in 50 of the 52 HCV isolates was specifically designed to overlap with previously obtained 5'NC sequences (Bukh et al. (1992b) Proc. Natl. Acad. Sci. U.S.A. 89:4942-4946) and with the E1 sequences disclosed herein at approximately 80 nucleotide positions each. A complete match was observed in 6033 of 6035 overlapping nucleotides. Two discrepancies were observed in isolate US6 at nt 552 (C and T) and nt 561 (C and T) respectively. This may have been due to microheterogeneity at these nucleotide positions, since the remaining overlapping sequence was unique for isolate US6. In addition, there were 3 confirmed instances of microheterogeneity: nt 33 in isolate SA11 (C,T and T), nt 36 in isolate S45 (A,C and A), and nt 552 in isolate P10 (C,T and T). Overall, the excellent agreement in these overlapping sequences in this study with the NC sequences disclosed in Bukh et al. and with the E1 sequences disclosed herein definitively ruled out contamination as a source of non-authentic HCV sequences. Furthermore, this analysis proved that the sequences obtained were from a single population, and not from different populations as could happen in mixed infections.

The core (C) gene was exactly 573 nucleotides in length in all 52 HCV isolates with an amino terminal start codon and no in-frame stop codons. Microheterogeneity was observed in 26 of the 52 HCV isolates at 0.2-1.4% of the 573 nucleotide positions of the C gene, and resulted in changes in 0.5-1.0% of the 191 predicted amino acids in 12 of these isolates. A multiple sequence alignment was performed and it showed that the nucleotide identities of the C gene among these HCV isolates were in the range of 79.4-99.0%. In order to compare the genetic relatedness of HCV isolates in different gene regions, phylogenetic trees of the C gene of all 52 HCV isolates and the E1 gene of 51 HCV isolates were constructed using the unweighted pair-

group method with arithmetic mean (Nei, M. (1987) Molecular Evolutionary Genetics (Columbia University Press, New York, N.Y., pp. 287-326) (Figure 8). In both dendrograms a division of the 45 HCV isolates from which C and E1 genes had been cloned into at least six major genetic groups (genotypes 1-6) and 12 minor genetic groups (genotypes I/1a, II/1b, III/2a, IV/2b, 2c, V/3a, 4a-4d, 5a, and 6a) was observed. It is noteworthy that a major division in genetic distance between HCV isolates of genotype 2 and those of the other genotypes in the phylogenetic analyses of both gene sequences was observed. Furthermore, the divergence of the minor genotypes within genotype 2 exhibited a degree of heterogeneity that is equivalent to that observed among the major genotypes. Analysis of the C gene from isolates Z5 and Z8, which had a unique 5' NC sequence (Bukh et al. (1992)) but from which the E1 gene could not be amplified, revealed that these isolates represented two additional genotypes. The designations 4e and 4f are assigned to these genotypes that have not been described previously. Overall, the present specification demonstrates that the genetic relatedness of HCV isolates is equivalent when analyzing the most conserved gene (C) and one of the most variable genes (E1) of the HCV genome, thereby providing strong evidence for the suggested division into major and minor genotypes.

Example 4

Computer Analysis of the Nucleotide and Deduced Amino Acid Sequences Of The Core Gene Of 52 HCV Isolates

In order to study further the heterogeneity of the C gene, a consensus sequence of the core gene from the 52 HCV isolates (Fig. 6J) was obtained. A total of 335 (58.5%) of the 573 nucleotides of the C gene were invariant among these HCV isolates. Nucleotides at the 1st and 2nd codon positions were invariant at 70.7% and 81.7% of these positions, respectively, while nucleotides at the 3rd

° position were invariant at only 23.0% of such positions. Stretches of 6 or more invariant nucleotides were observed from nucleotides 1-8, 22-27, 85-92, 110-125, 131-141, 334-340, 364-371, 397-404, and 511-516 and may be suitable for anchoring primers for amplification of HCV RNA in cDNA PCR assays.

Genotype-specific nucleotide positions of the core gene of hepatitis C virus were also noted for each of the genotypes. These genotype-specific nucleotides are shown below where each genotype-specific nucleotide is given in parentheses next to the nucleotide position in which it is found.

Genotype 1: 460 (C), 466 (C), 483 (C), 486 (G).

Genotype I/1a: 180 (T).

Genotype II/1b: 106 (C), 273 (G).

Genotype 2: 192 (C), 201 (A), 203 (A), 207 (G), 210 (C), 221 (A), 231 (A), 232 (A), 341 (A).

Genotype III/2a: 315 (C), 355 (G).

Genotype IV/2b: 45 (A), 174 (G), 216 (C), 348 (A), 376 (A), 414 (T).

Genotype 2c: 233 (G), 312 (C), 318 (A), 456 (C), 462 (G), 543 (C), 556 (T).

Genotype V/3a: 47 (T), 84 (A), 106 (G), 126 (A), 150 (T), 212 (G), 216 (A), 300 (A), 491 (T), 559 (C), 560 (A), 568 (G), 571 (A), 572 (G).

Genotype 4: 59 (T).

Genotype 4a: 213 (A), 231 (G), 415 (A).

° Genotype 4b: 66 (G), 145 (G), 310 (A).

Genotype 4c: 213 (T), 219 (A), 270 (T).

Genotype 4d: 212 (T), 327 (G), 469 (C).

5

Genotype 4e: 199 (C), 306 (A), 326 (A).

Genotype 4f: 57 (T), 75 (A), 267 (A).

10 Genotype 5a: 291 (G), 294 (C).

Genotype 6a: 59 (C), 175 (A), 195 (A), 198 (A), 214 (C),
224 (A), 316 (C), 351 (G), 387 (G), 444-447 (GGCT), 450
(G), 471-472 (AA), 474 (C).

15

These genotype-specific nucleotides are of utility in designing the genotype-specific PCR primers and hybridization probes.

20

Finally, although the full length nucleic acid sequence of the C gene of isolates representing genotypes I/1a, II/1b, III/2a, IV/2b and V/3a have been reported by others, those of 9 of the 14 genotypes (i.e., 2c, 4a-4f, 5a and 6a) have not been reported previously. In sum, by aligning the consensus sequences of the major genotypes, the present application enables those skilled in the art to map universally conserved sequences as well as genotype-specific sequences of the C gene among 14 genotypes of HCV.

25

In order to study the heterogeneity of the deduced C protein, a multiple sequence alignment of the predicted amino acids for all 52 HCV isolates was performed, and a consensus sequence was obtained (Fig. 7J). The identities of the predicted 191 amino acids of the C protein among these HCV isolates were in the range of 85.3-100.0%. A total of 132 (69.1%) of the 191 amino acids of the C protein were invariant. The most prevalent amino acids in the consensus sequence were glycine (13.6%),

35

arginine (12.6%), proline (11.0%), and leucine (9.9%). The most conserved amino acids were tryptophan (5 of 5 amino acids invariant), aspartic acid (5 of 5 amino acids invariant), proline (19 of 21 amino acids invariant) and glycine (23 of 26 amino acids invariant). Previous analyses indicated that HCV is evolutionarily related to pestiviruses (Miller et al. (1990) Proc. Natl. Acad. Sci. U.S.A. 87:2057-2061). In this regard, it is of interest to note that the C proteins of both viruses have a high content of proline residues (Collette M.S. et al. (1988) Virology 165:200-208), which are likely to be important in maintaining the structure of this protein. As is characteristic for a protein that binds to nucleic acid, the C protein has conserved amino acids that are basic and positively charged, and these are capable of neutralizing the negative charge of the HCV RNA encapsidated by this protein (Rice, C.M. et al. (1986) in *Togaviridae* and *Flaviviridae*, eds Schleinger, S. & Schlensinger, M.J. (Plenum Press, New York, N.Y.) pp. 279-326). Specifically, over 16% of the amino acids in the consensus sequence of the C protein of HCV are arginine and lysine that are located primarily in three clusters (i.e., from amino acids 6-23, 39-74 and 101-121) (Shih, C.M. et al. (1993) J. Gen. Virol. 67:5823-5832) (Fig. 7J). The 10 arginine and lysine residues within amino acids 39-62 are invariant among all 52 HCV isolates, suggesting that this domain may represent an important RNA-binding site. The capsid proteins of the related flavi- and pestiviruses (Miller et al. (1990)) also have a high content of arginine and lysine (Rice et al. (1986); Collette et al. (1988)). Although there are three major hydrophilic regions (i.e., amino acids 2-23, 39-74 and 101-121) that are conserved in all 52 HCV isolates, the remainder of the C protein is hydrophobic. Interestingly, one such highly conserved hydrophobic domain from aa 24-39 is flanked by proline residues. The hydrophobic domains are likely to be

° involved in protein-protein and/or protein-RNA interactions during assembly of the nucleocapsid, as well as in interaction with the lipoprotein envelope, as has been suggested for flaviviruses (Rice et al. (1986)). Other significant observations are: (i) a cluster of 5 invariant
5 tryptophan residues from aa 76-107; (ii) the lack of an N-linked glycosylation site (N-X-T/S); (iii) two potential nuclear localization signals (i.e., PRRGPR at amino acids 38-43 and PRGRRQP at amino acids 58-64) that are present in all 52 HCV isolates (Shih et al. (1993)); and (iv) a
10 putative DNA-binding motif SPRG at amino acids 99-102, found in 51 of the 52 HCV isolates, with SP present in all 52 isolates. This study demonstrates that the C protein has features that are highly conserved among the various genotypes of HCV, and that are known to be characteristic
15 of capsid proteins of other related viruses.

It should also be noted that the phylogenetic analysis of the amino acid sequence of the C proteins was not capable of resolving the minor groups within genotypes 1 and 4 because of the conservation of this protein (data
20 not shown). Indeed, only a few type-specific amino acids were identified. One striking example was that isolates of genotype 4 have an additional methionine at position 20 that is specific for this major genetic group. Finally, the conservation of the sequences surrounding the cleavage
25 site between the C and the E1 proteins of the different genotypes, which has been determined to be between amino acid 191 (alanine) and aa 192 (tyrosine) in HCV isolates of genotype 1 was analyzed (Hijikata, M., et al. (1991) Proc. Natl. Acad. Sci. USA 88:5547-5551). The C-terminal
30 sequence of C is serine-alanine in all but one of the 48 HCV isolates comprising genotypes 1, 2, 4, 5 and 6. However, all 4 HCV isolates of genotype 3 in this study, as well as isolates of genotype 3 published previously (Okamoto, H., et al. (1993) *J. Gen. Virol.* 74:2385-2390, Stuyver, L., et al. (1993) *Biochem. Biophys. Res. Comm.*
35

- ° 192:635-641), contain alanine-serine at this position. Thus, studies will be needed to determine the C/E1 cleavage site in genotype 3 isolates. Overall, the present invention application discloses the mapping of universally conserved sequences, as well as genotype-specific sequences, of the C protein among 14 genotypes of HCV.

Implications of the mapping of universally conserved and genotype-specific core nucleotide and amino acid core sequences for diagnosis of HCV infection and for determination of HCV genotypes

- 10 Detection of antibodies directed against the HCV core protein is important in the diagnosis of HCV infection. The recombinant C22-3 protein, spanning amino acids 2-120 of the C gene, is a major component of the commercially available second-generation anti-HCV tests.
- 15 Several studies have indicated that the three major hydrophilic regions of the C protein contain linear immunogenic epitopes (summarized in J. Clin. Microbiol., 30:1989-1994) (Sällberg, M. et al. (1992)). For example, antibodies against synthetic peptides from amino acids 1-
- 20 18, 51-68 and 101-118 were detected in infected patients (Sällberg, M. et al. (1992)). The present application demonstrates that, while these immunogenic regions are highly conserved, genotype-specific differences are observed at several amino acid positions that may influence
- 25 the specificity and sensitivity of the serological tests. One such example is that a single amino acid substitution at amino acid 110 has been demonstrated to affect seroreactivity (Sällberg, et al. (1992)). Despite the high degree of conservation in the immunodominant regions of the
- 30 C protein among the different genotypes, it is possible that genetic heterogeneity of the C protein could lead to false negative results in current serological tests.

- 35 With respect to genotype analysis, several methods have been used to determine the genotype of HCV isolates without resorting to sequence analysis. These

- ° include PCR followed by: (i) amplification with type-specific primers (Okamoto, H. et al. (1992) J. Gen. Virol., 73:673-679); (ii) determination of restriction-length polymorphism (Simmons, P. et al. (1993) J. Gen. Virol., 74:661-668); and (iii) specific hybridization (Stuyver, L. (1993) J. Gen. Virol., 74:1093-1102). The proposed methods have primarily been based on 5' NC and C sequences. Previous studies suggested that 5' NC-based genotyping systems would only be predictive of the major genetic groups of HCV (Bukh, J., et al. (1992) Proc. Natl. Acad. Sci. USA 89:4942-4946, Bukh, J., et al. (1993) Proc. Natl. Acad. Sci. USA 90:8234-8238). The most widely used C-based genotype system has been the PCR assay with type-specific primers that was designed for distinguishing HCV isolates of genotypes I/1a, II/1b, III/2a, IV/2b and V/3a (Okamoto, H., et al. (1993) J. Gen. Virol. 74:2385-2390, Okamoto, H. et al. (1992) J. Gen. Virol. 73:673-679). Since this system was developed prior to the identification of genotypes 2c, 4a-4f, 5a and 6a there are significant limitations to this typing system. For example, the primers specific for genotype IV/2b (nt 270-251) are as highly conserved within isolates of genotype 4c and 6a as within the isolates of genotype IV/2b. Thus, this assay probably can not distinguish among these genotypes. Another C-based approach involves distinguishing between genotypes 1 and 2 by type-specific antibody responses (Machida et al (1992) Hepatology, 16:886-891). Synthetic peptides composed of amino acids 65-81 were found to be genotype-specific for genotypes 1 and 2 in ELISA assays. The present analysis of amino acid sequences demonstrated significant variation within isolates of genotypes 1 and 2. Thus it is likely that these peptides will not identify all isolates of genotypes 1 and 2. Furthermore, the peptide for genotype 1 was highly conserved within isolates of genotypes 3 and 4 and might detect antibodies against these genotypes as well. Finally, it should be pointed out that

- ° most isolates of genotypes 3 and 4 had an identical amino acid sequence at positions 65-81.

Example 5

Detection by ELISA Based on Antigen from 5 Insect Cells Expressing Complete E1 Or Core Protein

Expression of E1 or Core protein in SF9 cells. A
cDNA (eg SEQ ID NO:1) encoding a complete E1 protein (eg
SEQ ID NO:52) or a cDNA (eg SEQ ID NO:103) encoding a
complete core protein (e.g. SEQ ID NO:155) is subcloned
10 into pBlueBac - Transfer vector (Invitrogen) using standard
subcloning procedures. The resultant recombinant
expression vector is cotransfected into SF9 insect cells
(Invitrogen) by the Ca precipitation method according to
the Invitrogen protocol.

15 ELISA Based on Infected SF9 cells. 5×10^6 SF9
cells infected with the above-described recombinant
expression vector are resuspended in 1 ml of 10 mM Tris-
HCl, pH 7.5, 0.15M NaCl and are then frozen and thawed 3
times. 10 ul of this suspension is dissolved in 10 ml of
20 carbonate buffer (pH 9.6) and used to cover one flexible
microtiter assay plate (Falcon). Serum samples are diluted
1:20, 1:400 and 1:8000, or 1:100, 1:1000 and 1:10000.
Blocking and washing solutions for use in the ELISA assay
are PBS containing 10% fetal calf serum and 0.5% gelatin
25 (blocking solution) and PBS with 0.05% Tween -20 (Sigma,
St.Louis, MO) (washing solution). As a secondary antibody,
peroxidase-conjugated goat IgG fraction to human IgG or
horse radish peroxidase-labelled goat anti-Old or anti-New
World monkey immunoglobulin is used. The results are
30 determined by measuring the optical density (O.D.) at 405
nm.

To determine if insect cells-derived E1 or core
protein representing genotype I/a of HCV could detect anti-
HCV antibody in chimpanzees infected with genotype I/1a of
HCV, three infected chimpanzees are examined. The serum of
35

- ° all 3 chimpanzees are found to seroconvert to anti-HCV.

Example 6

Use of the Complete E1 Protein as a Vaccine

- 5 Mammals are immunized with purified or partially purified E1 protein in an amount sufficient to stimulate the production of protective antibodies. The immunized mammals challenged with various genotypes of HCV are protected.
- 10 It is understood by one skilled in the art that the recombinant E1 protein used in the above vaccine can also be used in combination with other recombinant E1 proteins having an amino acid sequence shown in SEQ ID NOS:52-102. In addition, recombinant core proteins having
- 15 an amino acid sequence shown in SEQ ID NOS:155-206 could also be used in the above vaccine, either alone, in combination with other recombinant core proteins of the present invention, or in combination with recombinant E1 proteins having an amino acid sequence shown in SEQ ID
- 20 NOS:52-102.

Example 7

Determination of the Genotype of an HCV Isolate Via Hybridization of Genotype-Specific Oligonucleotides to RT-PCR Amplification Products.

- 25 Viral RNA is isolated from serum obtained from a mammal and is subjected to RT-PCR as in Example 1 or Example 3. Following amplification, the amplified DNA is purified as described in Example 1 or Example 3 and
- 30 aliquots of 100 ul of amplification product are applied to dots on a nitrocellulose filter set in a dot blot apparatus. The dots are then cut into separate dots and each dot is hybridized to a ³²P-labelled oligonucleotide specific for a single genotype of HCV. The
- 35 oligonucleotides to be used as hybridization probes are

- ° deduced from the consensus sequences shown in Figures 1A-1H or 6A-6J or from the SEQ ID NOs: representing E1 or core sequences comprising genotypes 4a-4f, 2c and 6a.

Example 8

5 ELISA Based on Synthetic Peptides Derived From E1 cDNA Sequences

E1 peptide(s) specific for genotype I/1a is placed in 0.1% PBS buffer and 50ul of a 1mg/ml solution of peptide is used to cover each well of the microtiter assay plate. Serum samples from two mammals infected with genotype I/1a HCV and from one mammal infected with genotype 5a HCV are diluted as in Example 3 and the ELISA is carried out as in Example 3. Both mammals infected with genotype I HCV react positively with peptides while the mammal infected with genotype 5a HCV exhibits no reactivity. One skilled in the art would readily understand that in the above experiment, core peptides specific for genotype I/1a could be used in place of, or in combination with the E1 genotype-specific peptide(s).

10

Example 9

Use of E1 Peptides as a Vaccine

Since the E1 genotype-specific peptides of the present invention are derived from two variable regions in the complete E1 protein, there exists support for the use of these peptides as a vaccine to protect against a variety of HCV genotypes. Mammals are immunized with peptide(s) selected from SEQ ID NOs: 136-159 in an amount sufficient to stimulate production of protective antibodies. The immunized mammals challenged with various genotypes of HCV are protected. One skilled in the art would readily understand that genotype-specific core peptides of the present invention could also be used either alone, in combination with each other, or in combination with the

35

- ° genotype-specific E1 peptides, as a vaccine to protect against a variety of HCV genotypes. In addition, the above vaccines may also be formulated using the universal core and/or E1 peptides of the present invention.

5

10

15

20

25

30

35

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: BUKH, J., MILLER, R.H. AND
PURCELL, R.H.
- 5 (ii) TITLE OF INVENTION: NUCLEOTIDE AND DEDUCED
AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND
CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE
SEQUENCES IN DIAGNOSTIC METHODS AND
VACCINES
- 10 (iii) NUMBER OF SEQUENCES: 263
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
15 (E) COUNTRY: USA
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1
- 20 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: TO BE ASSIGNED
(B) FILING DATE: 26-MAY-1998
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/290,665
(B) FILING DATE: 15-AUG-1994
- 25 (viii) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/086,428
(B) FILING DATE: 29-JUNE-1993
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: RICHARD W. BORK
(B) REGISTRATION NUMBER: 36,459
30 (C) REFERENCE/DOCKET NUMBER: 2026-4116US2
- (x) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 758-4800
(B) TELEFAX: (212) 751-6849
(C) TELEX: 421792

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosaapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10	TAC CAA GTG CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAC TCG AGT ATC GTG TAC GAG GCG GCC	78
	GAT GCC ATC CTG CAC ACT CCG GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC GTC TCG AGG TGT TGG GTG GCG ATG ACC	156
	CCC ACG GTG GCC ACC AGG GAT GGC AAA CTC CCC ACA GCG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTC GTC GGG AGT GCC	234
	ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG	273
	TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC	312
15	AGG CGC CAC TGG ACG ACG CAA GGC TGC AAT TGT TCT ATC	351
	TAT CCT GGC CAT ATA ACG GGT CAC CGC ATG GCG TGG GAT	390
	ATG ATG ATG AAC TGG TCC CCT ACC ACG GCG TTG GTA GTA	429
	GCT CAG CTG CTC CGG ATC CCG CAA GCC ATC TTG GAC ATG	468
	ATC GCT GGT GCT CAC TGG GGA GTC CTG GCG GGC ATA CCG	507
	TAT TTT TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA	546
20	GTG CTG CTG CTA TTT GCC GGC GTC GAC GCG	576

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosaapiens
 (C) INDIVIDUAL ISOLATE: DK9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

30	TAC CAA GTA CGC AAC TCC TCG GGC CTC TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC	78
	GAT GCC ATC CTG CAT TCT CCA GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC GCC TCG AAA TGT TGG GTG GCG GTG GCC	156
	CCC ACG GTG GCC ACC AGG GAC GGC AAG CTC CCC GCA ACG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC	234
	ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC TTG TGC GGG	273

TCT GTC TTC CTT GTC GGC CAA CTG TTC ACC TTC TCC CCC 312
 AGA CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC 351
 TAC CCC GGC CAT ATT ACG GGT CAT CGC ATG GCG TGG GAT 390
 ATG ATG ATG AAC TGG TCC CCT ACA GCA GCG CTG GTA ATG 429
 GCG CAG CTG CTC AGG ATC CCG CAG GCC ATC TTG GAC ATG 468
 ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
 5 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC GTG GTG 546
 GTA CTG TTG CTG TTT ACC GGC GTC GAT GCG 576

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR1

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CAC CAA GTG CGC AAC TCT ACA GGG CTT TAC CAT GTC ACC 39
 AAT GAT TGC CCT AAT TCG AGT ATT GTG TAC GAG GCG GCC 78
 GAT GCC ATC CTG CAC GCG CCG GGG TGT GTC CCT TGC GTT 117
 CGC GAG GGT AAC GCC TCG AGG TGT TGG GTG GCG GTG ACC 156
 CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG 195
 20 CAG CTT CGA CGT CAC ATC GAC CTG CTT GTC GGG AGC GCC 234
 ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC CTG TGC GGG 273
 TCT GTC TTC CTT GTC GGT CAA CTG TTC ACC TTT TCT CCC 312
 AGG CGC CAC TGG ACA ACG CAA GAC TGC AAT TGT TCT ATC 351
 TAT CCC GGC CAT ATA ACG GGA CAC CGT ATG GCA TGG GAT 390
 ATG ATG ATG AAC TGG TCC CCT ACG ACA GCG CTG GTA ATG 429
 GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468
 ATC GCT GGA GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
 25 TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC GTG GTA 546
 GTG CTG TTG CTG TTT GCC GGC GTT GAT GCG 576

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

	CAC	CAA	GTG	CGC	AAC	TCT	ACA	GGG	CTT	TAC	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAT	TCG	AGT	ATT	GTG	TAC	GAG	GCG	GCC	78
	GAT	GCC	ATC	CTG	CAC	ACG	CCG	GGG	TGT	GTC	CCT	TGC	GTT	117
5	CGC	GAG	GGT	AAC	ACC	TCG	AGG	TGT	TGG	GTG	GCG	GTG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	ACA	ACG	195
	CAG	CTC	CGA	CGT	CAC	ATC	GAC	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGC	TCG	GCC	CTC	TAC	GTG	GGG	GAC	TTG	TGC	GGG	273
	TCT	GTC	TTC	CTT	GTC	GGT	CAA	CTG	TTC	ACC	TTC	TCT	CCC	312
	AGG	CAC	CAC	TGG	ACA	ACG	CAA	GAC	TGC	AAT	TGT	TCC	ATC	351
	TAT	CCC	GGC	CAT	ATA	ACG	GGC	CAC	CGC	ATG	GCG	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	ACA	GCG	CTG	GTA	GTA	429
10	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAC	ATG	468
	ATC	GCT	GGT	GCC	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGG	AAC	TGG	GCG	AAG	GTC	CTG	GTA	546
	GTG	CTG	TTG	CTG	TTT	GCC	GGC	GTT	GAT	GCG				576

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	TAC	CAA	GTG	CGC	AAC	TCC	ACG	GGG	CTT	TAC	CAT	GTT	ACC	39
	AAT	GAT	TGC	CCT	AAC	TCG	AGT	ATT	GTG	TAC	GAG	ACA	GCT	78
	GAT	GCT	ATC	CTA	CAC	GCT	CCG	GGA	TGT	GTC	CCT	TGC	GTT	117
25	CGT	GAG	GGT	AAC	ACC	TCG	AGG	TGT	TGG	GTG	GCG	ATG	ACC	156
	CCC	ACG	GTG	GCC	ACC	AGG	GAC	GGC	AAA	CTC	CCC	GCA	ACG	195
	CAG	CTT	CGA	CGT	TAC	ATC	GAT	CTG	CTT	GTC	GGG	AGC	GCC	234
	ACC	CTC	TGT	TCG	GCC	CTC	TAC	GTG	GGG	GAC	TTG	TGC	GGG	273
	TCT	GTC	TTT	CTT	GTC	GGT	CAG	CTG	TTT	ACC	TTC	TCT	CCC	312
	AGG	CGC	CTC	TGG	ACG	ACG	CAA	GAC	TGC	AAT	TGT	TCT	ATC	351
	TAT	CCC	GGC	CAT	ATA	ACG	GGT	CAT	CGC	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCC	CCT	ACG	ACG	GCA	CTG	GTA	GTA	429
30	GCT	CAG	CTG	CTC	CGG	ATC	CCA	CAA	GCC	ATC	TTG	GAT	ATG	468
	ATC	GCT	GGT	GCT	CAC	TGG	GGA	GTC	CTA	GCG	GGC	ATA	GCG	507
	TAT	TTC	TCC	ATG	GTG	GGA	AAC	TGG	GCG	AAG	GTC	CTA	GTG	546
	GTG	CTG	CTG	CTA	TTC	GCC	GGC	GTT	GAC	GCG				576

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

10	TAC CAA GTA CGC AAC TCC ACG GGC CTT TAC CAT GTC ACC	39
	AAT GAC TGC CCT AAC TCG AGC ATT GTG TAC GAG ACG GCC	78
	GAT ACC ATC CTA CAC TCT CCG GGG TGT GTC CCT TGC GTT	117
	CGC GAG GGT AAC GCC TCG AGA TGT TGG GTG CCG GTG GCC	156
	CCC ACA GTT GCC ACC AGG GAC GGC AAA CTC CCC GCA ACG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTT GGG AGC GCC	234
	ACC CTC TGC TCG GCC CTC TAT GTG GGG GAC CTG TGC GGG	273
	TCT GTC TTT CTT GTC AGC CAG CTG TTC ACT ATC TCC CCC	312
15	AGG CGC CAC TGG ACA ACG CAA GAC TGC AAC TGT TCT ATC	351
	TAC CCC GGC CAT ATA ACG GGT CAC CGT ATG GCA TGG GAT	390
	ATG ATG ATG AAC TGG TCC CCT ACA ACG GCG TTG GTA ATA	429
	GCT CAG CTG CTC AGG GTC CCG CAA GCC GTC TTG GAC ATG	468
	ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG	507
	TAT TTC TCC ATG GCG GGG AAC TGG GCG AAG GTC CTG CTA	546
	GTG CTG TTG CTG TTT GCC GGC GTC GAT GCG	576

20 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

30	TAC CAA GTA CGC AAC TCC TCG GGC CTT TAC CAT GTC ACC	39
	AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG ACG GCC	78
	GAT GCC ATT CTA CAC TCT CCA GGG TGT GTC CCT TGC GTT	117
	CGC GAG GAT GGC GCC CCG AAG TGT TGG GTG GCG GTG GCC	156
	CCC ACA GTC GCC ACT AGG GAC GGC AAA CTC CCT GCA ACG	195
	CAG CTT CGA CGT CAC ATC GAT CTG CTT GTC GGA AGC GCC	234
	ACC CTC TGC TCG GCC CTC TAC GTG GGG GAC TTG TGC GGG	273
35	TCT GTC TTT CTC GTC AGT CAA CTG TTC ACG TTC TCC CCC	312

0

```

AGG CGC CAC TGG ACA ACG CAA GAC TGT AAC TGT TCT ATC 351
TAT CCC GGC CAC ATA ACG GGT CAC CGC ATG GCA TGG GAT 390
ATG ATG ATG AAC TGG TCC CCC ACA ACA GCG CTG GTA GTA 429
GCT CAG CTG CTC AGG ATC CCG CAA GCC GTC TTG GAC ATG 468
ATC GCT GGT GCC CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG ATA 546
5 GTG CTG TTG CTG TTT TCC GGC GTC GAT GCG 576

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15

```

TAC CAA GTA CGC AAC TCC ACG GGG CTT TAC CAT GTC ACC 39
AAT GAT TGC CCT AAC TCG AGT ATT GTG TAC GAG GCG GCC 78
GAT GCC ATC CTG CAC ACT CCG GGG TGT GTT CCT TGC GTT 117
CGC GAG GGT AAC GCT TCG AGG TGT TGG GTG GCG ATG ACC 156
CCC ACG GTG GCC ACC AGG GAC GGC AAA CTC CCC ACA ACG 195
CAA CTT CGA CGT CAC ATC GAT CTG CTT GTC GGG AGC GCC 234
20 ACC CTC TGT TCG GCC CTC TAC GTG GGG GAC CTG TGG GGC 273
TCT GTC TTT CTT GTC GGT CAA CTG TTT ACC TTC TCT CCC 312
AGA CGC CAC TGG ACG ACG CAG GGC TGC AAT TGT TCT ATC 351
TAT CCC GGC CAT ATA ACG GGT CAC CGC ATG GCA TGG GAT 390
ATG ATG ATG AAC TGG TCC CCT ACG GCG GCG TTG GTG GTA 429
GCT CAG CTG CTC CGG ATC CCA CAA GCC ATC TTG GAC ATG 468
ATC GCT GGT GCT CAC TGG GGA GTC CTA GCG GGC ATA GCG 507
TAT TTC TCC ATG GTG GGG AAC TGG GCG AAG GTC CTG GTA 546
25 GTG CTG CTG CTA TTT GCC GGC GTC GAC GCG 576

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

35

5
10
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG 39
AAC GAC TGT TCC AAC TCG AGC ATT GTG TAT GAG ACA GCG 78
GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT 117
CGG GAG GAC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACC 156
CCC ACG CTC GCG GCT AGG AAT GGC AAC GTC CCC ACT ACG 195
GCG ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
GCT TTC TGC TCC GCC ATG TAC GTG GGG GAT CTC TGC GGA 273
TCT GTT TTC CTC ATC TCC CAG CTG TTC ACC CTC TCG CCT 312
CGC CGG CAT GAG ACG GTA CAG GAG TGT AAT TGC TCA ATC 351
TAT CCC GGC CAC GTG ACA GGT CAC CGT ATG GCT TGG GAT 390
ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC TTA GTG GTA 429
TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTC GCC 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
GTG ATG CTA CTC TTT GCT GGC GTT GAC GGC 576

(2) INFORMATION FOR SEQ ID NO:10:

15
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D3

20
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25
30
TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAA GTC ACC 39
AAT GAC TGT TCC AAC TCG AGC ATC GTG TAT GAG ACA GCG 78
GAC ATG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT 117
CGG GAG GAC AAC TCC TCT CGC TGC TGG GTA GCG CTC ACC 156
CCC ACG CTC GCG GCT AGG AAT AGC AGC GTC CCC ACT ACG 195
ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
GCT TTC TGC TCC GCC ATG TAC GTG GGG GAT CTT TGC GGA 273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT 312
CGC CGG CAT GAG ACA GTA CAG GAA TGT AAC TGC TCA ATC 351
TAT CCC GGC CAC GTG ACA GGT CAC CGC ATG GCT TGG GAT 390
ATG ATG ATG AAC TGG TCG CCT ACA GCA GCC CTA GTG GTA 429
TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTC GCC 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
GTG ATG CTA CTC TTT GCT GGC GTC GAC GGC 576

(2) INFORMATION FOR SEQ ID NO:11:

35
(i) SEQUENCE CHARACTERISTICS:

o

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAC	GTC	ACA	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATC	GTG	TAT	GAG	GCA	GTG	78
10	GAC	GTG	ATC	ATG	CAT	ACC	CCA	GGG	TGC	GTG	CCC	TGC	GTT	117
	CGG	GAG	AAC	AAC	CAC	TCC	CGT	TGC	TGG	GTA	GCG	CTC	ACC	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GCC	AGC	ATC	CCC	ACT	ACG	195
	ACA	ATA	CGA	CGC	CAT	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCT	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	273
	TCC	GTT	TTC	CTC	GTC	TCT	CAG	CTG	TTC	ACC	TTT	TCA	CCT	312
	CGC	CGG	CAT	GAG	ACA	GCA	CAG	GAC	TGC	AAC	TGC	TCA	ATC	351
	TAT	CCC	GGC	CAC	GTT	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
15	ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCC	CTA	GTG	CTA	429
	TCG	CAG	TTA	CTC	CGA	ATC	CCA	CAA	GCT	GTC	GTG	GAG	ATG	468
	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTG	GCG	GGC	CTC	GCC	507
	TAC	TAC	TCC	ATG	GCG	GGG	AAC	TGG	GCC	AAG	GTT	TTA	ATT	546
	GTG	TTG	CTA	CTC	TTT	GCC	GGC	GTT	GAT	GGG				576

(2) INFORMATION FOR SEQ ID NO:12:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

25 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

	TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATA	TAC	CAT	GTC	ACG	39
	AAC	GAC	TGC	TCC	AAC	TCA	AGC	GTC	GTG	TAT	GAG	ACA	GCA	78
30	GAC	ATG	ATC	ATG	CAT	ACC	CCT	GGA	TGC	GTG	CCC	TGC	GTA	117
	CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGT	TGG	GTA	GCG	CTC	ACT	156
	CCC	ACG	CTC	GCG	GCC	AGG	AAC	GTC	AGC	GTC	CCC	ACC	ACG	195
	ACA	ATA	CGA	CGT	CAC	GTC	GAC	TTG	CTC	GTT	GGG	GCG	GCT	234
	GCC	TTC	TGC	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
	TCT	GTT	TTC	CTT	GTC	TCC	CAG	CTG	TTC	ACC	TTT	TCG	CCT	312
	CGC	CGA	CAC	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGC	TCA	CTC	351
35	TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390

ATG ATG ATG AAC TGG TCC CCT ACA GCA GCC CTA GTG GTG 429
TCG CAA TTA CTC CGG ATC CCG CAA GCT GTC GTG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTA GCG GGC CTT GCC 507
TAC TAT TCC ATG GTG GGA AAC TGG GCT AAG GTT TTG ATT 546
GTG ATG CTA CTT TTT GCC GGC GTT GAT GGG 576

5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

15 CAT GAA GTG CAC AAC GTA TCC GGG ATC TAC CAT GTC ACG 39
AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG 78
GAC ATG ATC ATG CAT ACC CCC GGG TGC GTG CCC TGC GTC 117
CGG GAG AAC AAC TCC TCC CGT TGC TGG GTA GCG CTC ACT 156
CCC ACG CTC GCG GCC AGG AAC GCC AGC ATC CCC ACT ACG 195
ACA ATA CGA CGC CAT GTC GAC TTG CTC GTT GGG GCG GCT 234
GCT TTC TGC TCC GCC ATG TAC GTG GGA GAT CTC TGC GGA 273
TCT GTC TTC CTC GTC TCC CAG TTG TTC ACC TTC TCG CCT 312
20 CGC CGG CAT GAG ACG GTA CAG GAC TGC AAT TGC TCA ATC 351
TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT 390
ATG ATG ATG AAC TGG TCA CCT ACA GCA GCC CTA GTG GTA 429
TCG CAG TTA CTC CGA CTC CCA CAA GCT GTC ATG GAC ATG 468
GTG GCG GGA GCC CAC TGG GGA GTC CTA GCG GGC CTT GCT 507
TAC TAT TCC ATG GTG GGG AAC TGG GCC AAG GTT TTG ATT 546
GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

25

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

35

5
 10
 TAT GAA GTG CGC AAC GTG TCC GGG GTA TAC CAT GTC ACG 39
 AAC GAC TGC TCC AAC TTA AGC ATC GTG TAC GAG ACA ACG 78
 GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT 117
 CGG GAA AAC AAC TCC TCC CGT TGT TGG GTA GCG CTC GCC 156
 CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACC ACG 195
 GCA ATA CGA CGC CAC GTC GAC TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTT TGC GGA 273
 TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTC TCG CCT 312
 CGC CGA CAC GAG ACG GTA CAG GAC TGC AAC TGC TCA ATC 351
 TAT CCC GGC CAC GTA ACA GGT CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCA CCT ACA ACA GCC CTA GTG GTG 429
 TCG CAG TTA CTC CGG ATC CCG CAA GCT GTC GTG GAC ATG 468
 GTA GCG GGG GCC CAC TGG GGG GTC CTG GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTG GGA AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTT TTT GCC GGC GTT GAT GGG 576

(2) INFORMATION FOR SEQ ID NO:15:

15
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK8

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25
 30
 TAT GAA GTG CGC AAC GTG TCC GGG ATA TAC CAT GTC ACG 39
 AAC GAC TGC TCC AAC TCA AGC ATC GTG TAT GAA ACA GCG 78
 GAC ATG ATT ATG CAT ACC CCT GGA TGC ATG CCC TGC GTT 117
 CGG GAG AAC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT 156
 CCC ACG CTC GCG GCT AGG AAT GTC AGC GTC CCC ACT ACG 195
 ACA ATA CGA CGC CAC GTC GAC TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273
 TCT GTT TTC CTC GTC TCC CAG CTG TTC ACC TTT TCG CCT 312
 CGC CGA CAC GAG ACG GTA CAG GAC TGC AAC TGC TCA ATC 351
 TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCG CCC ACA ACA GCC CTA GTG GTG 429
 TCG CAG TTA CTC CGG ATC CCG CAA GCT ATC GTG GAC ATG 468
 GTG GCG GGG GCC CAC TGG GGA GTC CTA GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTG GGC AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTG TTT GCC GGC GTT GAT GGG 576

(2) INFORMATION FOR SEQ ID NO:16:

35
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
GAC	ATG	ATC	ATG	CAC	ACT	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
CGG	GAG	GGC	AAC	TCC	TCT	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
CCC	ACT	CTC	GCG	GCC	AGG	AAC	GCC	AGC	GTC	TCC	ACC	ACG	195
ACA	ATA	CGA	CAC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTA	TGC	GGA	273
TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCA	CCG	312
CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGC	TCC	ATC	351
TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCC	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCA	GCC	CTA	GTG	GTA	429
TCG	CAG	TTG	CTC	CGG	ATC	CCA	CAA	GCT	GTC	GTG	GAT	ATG	468
GTG	GCG	GGG	GCC	CAC	TGG	GGA	ATC	CTG	GCG	GGC	CTT	GCC	507
TAC	TAT	TCC	ATG	GTA	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
GTG	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TAT	GAG	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGT	ATT	GTG	TAT	GAG	GCA	GCG	78
GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
CGG	GAG	GGC	AAC	TTC	TCT	AGT	TGC	TGG	GTA	GCG	CTC	ACT	156
CCC	ACT	CTC	GCG	GCT	AGG	AAC	GCC	AGC	GTC	CCC	ACC	ACG	195
ACA	ATA	CGA	CGC	CAC	GTC	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
GCT	TTC	TGT	TCC	GCT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
TCT	GTT	TTC	CTT	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCA	CCG	312
CGC	CGG	CAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGC	TCC	ATC	351
TAT	CCC	GCG	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCG	GCC	CTA	GTG	GTA	429

TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAT ATG 468
 GTG GCG GGG GCC CAC TGG GGA ATC CTG GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTA GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

5 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

15 TAT GAA GTG CGC AAC GTG TCC GGG GTG TAC CAT GTC ACG 39
 AAC GAC TGC TCC AAC TCA AGT ATT GTG TAT GAG GCA GCG 78
 GAC ATG ATA ATG CAC ACC CCC GGG TGC GTG CCC TGT GTT 117
 CGG GAG AAC AAC TCC CGC TGC TGG GTA GCG CTC ACT 156
 CCC ACA CTC GCG GCT AGG AAT TCC AGC GTC CCA ACT ACG 195
 GCA ATA CGA CGC CAT GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273
 TCT GTT CTC CTC GTC TCC CAG CTG TTC ACC TTC TCA CCT 312
 CGC CGG CAT TGG ACA GTA CAG GAC TGC AAT TGT TCA ATC 351
 20 TAT CCT GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCG CCC ACA GCA GCC CTA GTG GTG 429
 TCG CAG CTA CTC CGG ATC CCA CAA GCT ATC TTG GAT GTG 468
 GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTC TTG ATT 546
 GTG ATG CTA CTC TTT GCC GGC GTT GAC GGA 576

25 (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

35 TAT GAA GTG CGC AAC GTA TCC GGG GCG TAC CAT GTC ACG 39

AAC GAC TGC TCC AAC TCA AGT ATT GTG TAC GAG GCA GCG 78
 GAC GTG ATC ATG CAT ACC CCC GGG TGT GTA CCC TGC GTT 117
 CAG GAG GGT AAC TCC CAA TGC TGG GTG GCG CTC ACC 156
 CCC ACG CTC GCG GCC AGG AAC GCT ACC GTC CCC ACC ACG 195
 ACA ATA CGA CGT CAT GTC GAT TTG CTC GTT GGG GCG GCT 234
 GTT TTC TGC TCC GCT ATG TAC GTG GGG GAC CTG TGC GGA 273
 TCT GTT TTC CTC ATC TCC CAG CTG TTC ACC ATC TCG CCC 312
 CGT CGG CAT GAG ACA GTA CAG AAC TGC AAT TGC TCA ATC 351
 TAT CCC GGA CAC GTG ACA GGT CAT CGC ATG GCC TGG GAT 390
 ATG ATG ATG AAC TGG TCG CCT ACA ACA GCC CTA GTG GTA 429
 TCG CAG CTA CTC CGG ATC CCA CAA GCT GTC ATG GAT ATG 468
 GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTC GCC 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
 GTG ATG CTA CTT TTT GCT GGT GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
- (C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAT GAA GTG CGC AAC GTG TCC GGG GCG TAC CAT GTC ACG 39
 AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GTG 78
 GAC GTG ATC CTG CAC ACC CCT GGG TGC GTG CCC TGC GTT 117
 CGG GAG AAC AAC TCC TCC CGT TGC TGG GTG GCG CTC ACT 156
 CCC ACG CTC GCG GCC AGG AAC TCC AGC GTC CCC ACT ACG 195
 ACA ATA CGA CGT CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273
 TCT GTT TTC CTT GTT TCC CAG CTG TTC ACC TTC TCG CCT 312
 CGT CGG CAT GAG ACA GTA CAG GAC TGC AAC TGT TCA ATC 351
 TAT CCC GGC CAC GTA ACA GGT CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAC TGG TCG CCT ACA GCA GCC TTA GTG GTA 429
 TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG 468
 GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT 546
 GTG ATG CTA CTC TTT GCC GGC GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 576 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: hom sapiens
 (C) INDIVIDUAL ISOLATE: SA10

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	ATG	TAC	CAT	GTC	ACG	39
AAC	GAC	TGC	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	GCA	GCG	78
GAC	ATG	ATC	ATG	CAC	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
CGG	GAG	AAC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
CCC	ACG	CTC	GCG	GCC	AGG	AAC	TCC	AGC	GTC	CCC	ACT	ACG	195
10	ACA	ATA	CGA	CGC	CAC	GTG	GAT	TTG	CTC	GTT	GGG	GCG	234
GCT	TTC	TGC	TCC	GCC	ATG	TAC	GTG	GGG	GAC	CTC	TGC	GGA	273
TCT	GTT	TTC	CTT	GTC	TCC	CAG	CTG	TTC	ACC	TTC	TCG	CCT	312
CGC	CGG	TAT	GAG	ACA	GTA	CAG	GAC	TGC	AAT	TGC	TCA	ATC	351
TAT	CCC	GGC	CGC	GTA	ACA	GGT	CAC	CGC	ATG	GCT	TGG	GAT	390
ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	ACA	GCT	CTA	GTA	GTA	429
TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	ATC	GTG	GAC	ATG	468
15	GTG	GCG	GGG	GCC	CAC	TGG	GGA	GTC	CTA	GCG	CTT	GCC	507
TAC	TAT	TCC	ATG	GTG	GGG	AAC	TGG	GCT	AAG	GTT	TTG	ATT	546
GTT	ATG	CTA	CTC	TTT	GCC	GGC	GTT	GAC	GGG				576

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: hom sapiens
 (C) INDIVIDUAL ISOLATE: SW2

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TAT	GAA	GTG	CGC	AAC	GTG	TCC	GGG	GTG	TAT	CAT	GTC	ACG	39
AAC	GAC	TGT	TCC	AAC	TCA	AGC	ATT	GTG	TAT	GAG	ACA	GCG	78
GAC	ATG	ATC	ATG	CAT	ACC	CCC	GGG	TGC	GTG	CCC	TGC	GTT	117
CGG	GAG	GCC	AAC	TCC	TCC	CGC	TGC	TGG	GTA	GCG	CTC	ACT	156
30	CCC	ACG	CTA	GCA	GCC	AGG	AAC	ACC	AGC	GTC	CCC	ACT	195
ACA	ATA	CGA	CGC	CAC	GTG	GAT	TTG	CTC	GTT	GGG	GCG	GCT	234
GCT	TTC	TGC	TCC	GTT	ATG	TAC	GTG	GGG	GAT	CTC	TGC	GGA	273
TCT	GTT	TTC	CTC	GTC	TCC	CAG	CTG	TTC	ACT	TTT	TCA	CCT	312
CGC	CGG	CAC	GAG	ACA	GTA	CAG	GAC	TGC	AAC	TGT	TCC	ATC	351
TAT	CCC	GGC	CAC	GTA	TCA	GGT	CAC	CGC	ATG	GCT	TGG	GAC	390
ATG	ATG	ATG	AAC	TGG	TCA	CCT	ACA	GCA	GCC	CTG	GTG	GTA	429
15	TCG	CAG	TTA	CTC	CGG	ATC	CCA	CAA	GCT	GTG	GAC	ATG	468

GTA GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCA 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
GTG ATG CTA CTC TTT GCT GGC GTT GAC GGG 576

(2) INFORMATION FOR SEQ ID NO:23:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TAC GAA GTG CGC AAC GTG TCC GGG GTG TAC TAT GTC ACG 39
AAC GAC TGT TCC AAC TCA AGC ATT GTG TAT GAG ACA GCG 78
15 GAC ATG ATC ATG CAC ACC CCT GGG TGC GTG CCC TGC GTT 117
CGG GAG AGC AAT TCC TCC CGC TGC TGG GTA GCG CTT ACT 156
CCC ACG CTC GCG GCC AGG AAC GCC AGC GTC CCC ACT AAG 195
ACA ATA CGA CGT CAC GTC GAC TTG CTC GTT GGG GCG GCT 234
GCT TTC TGT TCC GCT ATG TAC GTG GGG GAT CTC TGC GGA 273
TCT GTT TTC CTC GTC TCC CAG CTG TTC ACT TTC TCG CCT 312
CGC CGG CAT GAG ACA GTA CAG GAC TGC AAC TGC TCA ATC 351
TAT CCC GGC CAC GTA ACA GGT CAC CGT ATG GCT TGG GAT 390
20 ATG ATG ATG AAC TGG TCG CCC ACA ACG GCA CTA GTG GTG 429
TCG CAG TTG CTC CGG ATC CCA CAA GCT GTC GTG GAC ATG 468
GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT TTG ATT 546
GTG CTG CTA CTC TTT GCC GGC GTT GAT GGG 576

(2) INFORMATION FOR SEQ ID NO:24:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
30 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG 39
AAC GAC TGC TCC AAC TCA AGC ATT GTG TTT GAG GCA GCG 78

35

GAC TTG ATC ATG CAC ACC CCC GGG TGC GTG CCC TGC GTT 117
 CGG GAG GGC AAC TCC TCC CGC TGC TGG GTA GCG CTC ACT 156
 CCC ACG CTC GCG GCC AGG AAC ACC AGC GTC CCC ACT ACG 195
 ACG ATA CGA CGC CAT GTC GAT TTG CTC GTT GGG GCG GCT 234
 GCT TTC TGC TCC GCT ATG TAT GTG GGA GAC CTC TGC GGA 273
 TCT GTT TTC CTC GTC TCT CAG CTG TTC ACC TTC TCG CCT 312
 CGC CGG CAT GAG ACT TTG CAG GAC TGC AAC TGC TCA ATC 351
 TAT CCC GGC CAT CTG TCA GGT CAC CGC ATG GCT TGG GAC 390
 ATG ATG ATG AAC TGG TCG CCT ACA ACA GCT CTA GTG GTG 429
 TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG 468
 GTG ACA GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
 TAC TAT TCC ATG GCG GGG AAC TGG GCT AAG GTT TTA ATT 546
 GTG ATG CTA CTC TTT GCC GGC GTT GAT GGG 576

10

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TAT GAA GTG CGC AAC GTG TCC GGG ATG TAC CAT GTC ACG 39
 AAC GAC TGC TCC AAC TCA AGC ATT GTG TAT GAG GCA GCG 78
 GAC ATG ATC ATG CAC ACT CCC GGG TGC GTG CCC TGT GTT 117
 CGG GAG AAC AAT TCC TCC CGC TGC TGG GTA GCG CTC ACT 156
 CCC ACG CTC GCG GCC AGG AAC GCT AGC GTC CCC ACT ACG 195
 ACA ATA CGA CGC CAC GTC GAT TTG CTC GTT GGG GCG GCT 234
 ACT TTC TGC TCC GCT ATG TAC GTG GGG GAC CTC TGC GGG 273
 TCC GTT TTC CTC ATC TCC CAG CTG TTC ACC TTC TCG CCT 312
 CGT CAG CAT GAG ACA GTA CAG GAC TGC AAT TGT TCA ATC 351
 TAT CCC GGC CAC GTA TCA GGT CAC CGC ATG GCT TGG GAT 390
 ATG ATG ATG AAT TGG TCA CCT ACA GCA GCC CTA GTG GTA 429
 TCG CAG TTA CTC CGG ATC CCA CAA GCT GTC ATG GAC ATG 468
 GTG GCG GGG GCC CAC TGG GGA GTC CTG GCG GGC CTT GCC 507
 TAC TAT TCC ATG GTG GGG AAC TGG GCT AAG GTT CTG ATT 546
 GTG TTG CTA CTC TTT GCC GGC GTT GAC GGG 576

30

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

35

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5	GCC	CAA	GTG	AGG	AAC	ACC	AGC	CGC	GGT	TAC	ATG	GTG	ACT	39
	AAC	GAC	TGT	TCC	AAT	GAG	AGC	ATC	ACC	TGG	CAG	CTC	CAA	78
	GCC	GCG	GTT	CTC	CAC	GTC	CCC	GGG	TGT	ATC	CCG	TGT	GAG	117
	AGG	CTG	GGA	AAT	ACA	TCC	CGA	TGC	TGG	ATA	CCG	GTC	ACA	156
	CCA	AAC	GTG	GCC	GTG	CGG	CAG	CCC	GGC	GCT	CTT	ACG	CAG	195
	GGC	TTG	CGG	ACG	CAC	ATC	GAC	ATG	GTT	GTG	ATG	TCC	GCC	234
10	ACG	CTC	TGC	TCT	GCC	CTC	TAC	GTG	GGG	GAC	CTC	TGC	GGC	273
	GGG	GTG	ATG	CTC	GCA	GCC	CAG	ATG	TTC	ATT	GTC	TCG	CCG	312
	CGA	CGC	CAC	TGG	TTT	GTG	CAA	GAA	TGC	AAT	TGC	TCC	ATC	351
	TAC	CCC	GGT	ACC	ATC	ACT	GGA	CAC	CGT	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACA	GCC	ACC	ATG	ATC	CTG	429
	GCG	TAC	GCG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	ATA	GAC	ATC	468
	ATC	GGC	GGG	GCT	CAC	TGG	GGC	GTC	ATG	TTT	GGC	TTG	GCC	507
	TAC	TTC	TCT	ATG	CAG	GGA	GCG	TGG	GCG	AAG	GTC	ATT	GTC	546
15	ATC	CTC	TTG	CTG	GCT	GCT	GGG	GTG	GAC	GCG				576

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

20	GCA	CAA	GTG	AAG	AAC	ACC	ACT	AAC	AGC	TAC	ATG	GTG	ACC	39
	AAC	GAC	TGT	TCT	AAT	GAC	AGC	ATC	ACT	TGG	CAG	CTC	CAG	78
	GCC	GCG	GTC	CTC	CAC	GTC	CCC	GGG	TGT	GTC	CCG	TGC	GAG	117
	AAA	ACG	GGA	AAT	ACA	TCT	CGG	TGC	TGG	ATA	CCG	GTT	TCA	156
	CCA	AAC	GTG	GCC	GTG	CGG	CAG	CCC	GGC	GCC	CTC	ACG	CAG	195
	GGC	TTG	CGG	ACG	CAC	ATT	GAC	ATG	GTT	GTG	ATG	TCC	GCC	234
30	ACG	CTC	TGC	TCT	GCT	CTT	TAC	GTG	GGG	GAC	CTC	TGC	GGC	273
	GGG	GTG	ATG	CTC	GCA	GCC	CAG	ATG	TTC	ATC	GTC	TCG	CCG	312
	CAA	CAT	CAC	TGG	TTT	GTG	CAA	GAC	TGC	AAT	TGC	TCT	ATC	351
	TAC	CCT	GGC	ACC	ATC	ACT	GGA	CAC	CGT	ATG	GCA	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACG	GCC	ACC	ATG	ATC	CTG	429
	GCG	TAC	GCG	ATG	CGC	GTT	CCC	GAG	GTC	ATC	TTA	GAC	ATC	468
35	GTT	AGC	GGG	GCA	CAC	TGG	GGC	GTC	ATG	TTC	GGC	TTG	GCC	507

TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC 546
ATC CTT CTG CTG GCC GCT GGG GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCC GAA GTG AAG AAC ACC AGT ACC AGC TAC ATG GTG ACA 39
AAT GAC TGT TCC AAC GAC AGC ATC ACC TGG CAA CTC CAG 78
GCC GCG GTC CTC CAC GTC CCC GGG TGC GTC CCG TGC GAG 117
AGA GTT GGA AAC GCG TCG CGG TGC TGG ATA CCG GTC TCG 156
CCA AAC GTA GCT GTG CAG CGG CCT GGC GCC CTC ACG CAG 195
GGC TTG CGG ACG CAC ATC GAC ATG GTT GTG ATG TCC GCC 234
ACG CTC TGC TCC GCT CTC TAC GTG GGG GAT CTC TGC GGC 273
GGG GTA ATG CTC GCC GCT CAG ATG TTC ATT ATC TCG CCG 312
CAG CAC CAC TGG TTT GTG CAG GAA TGC AAC TGC TCC ATT 351
TAC CCT GGT ACC ATC ACT GGA CAC CGT ATG GCA TGG GAC 390
ATG ATG ATG AAC TGG TCG CCC ACA ACC ACC ATG ATC TTG 429
GCG TAC GCG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468
ATC AGC GGA GCT CAC TGG GGC GTC ATG TTC GGC CTA GCC 507
TAC TTC TCT ATG CAG GGA GCG TGG GCG AAG GTC GTT GTC 546
ATC CTG TTG CTC ACC GCT GGC GTG GAC GCG 576

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTC CAA GTG AAA AAC ACC AGT ACC AGC TAT ATG GTG ACC 39
AAT GAC TGC TCC AAC GAC AGC ATC ACT TGG CAA CTT GAG 78
GCT GCG GTC CTC CAC GTT CCC GGG TGT GTC CCG TGC GAG 117

AAA GTG GGA AAT ACA TCT CGG TGC TGG ATA CCG GTC TCA 156
 CCA AAT GTG GCC GTG CAG CGG CCT GGC GCC CTC ACG CAG 195
 GGC TTG CGG ACT CAC ATC GAC ATG GTC GTG ATG TCC GCC 234
 ACG CTC TGC TCC GCT CTT TAC GTG GGG GAC TTC TGC GGT 273
 GGG ATG ATG CTC GCA GCC CAA ATG TTC ATT GTC TCG CCG 312
 CGC CAC CAC TCG TTT GTG CAG GAA TGC AAC TGC TCC ATC 351
 TAC CCC GGT ACC ATC ACC GGC CAC CGT ATG GCA TGG GAC 390
 5 ATG ATG ATG AAC TGG TCG CCC ACG GCC ACT TTG ATC CTG 429
 GCG TAC GTG ATG CGC GTT CCC GAG GTC ATC ATA GAC ATC 468
 ATT AGC GGG GCG CAT TGG GGC GTC TTG TTC GGC TTA GCC 507
 TAC TTC TCT ATG CAG GGA GCG TGG GCG AAA GTC GTT GTC 546
 ATC CTT CTG CTA GCC GCT GGG GTG GAC GCG 576

10 (2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GTG GAA GTC AGG AAC ATC AGT TCC AGC TAC TAC GCC ACC 39
 20 AAT GAT TGC TCA AAC AAC AGC ATC ACC TGG CAA CTC ACC 78
 GAC GCA GTT CTC CAC CTT CCC GGA TGC GTC CCA TGT GAG 117
 AAT GAC AAT GGC ACC CTG CGC TGC TGG ATA CAA GTG ACA 156
 CCT AAT GTG GCT GTG AAA CAC CGC GGC GCA CTT ACT CAT 195
 AAC CTG CGA ACA CAC GTC CAG GTG ATC GTA ATG GCA GCT 234
 ACG GTC TGC TCG GCC TTG TAT GTG GGA GAC GTA TGC GGG 273
 GCC GTG ATG ATC GTG TCG CAG GCT CTC ATA ATA TCG CCT 312
 GAA CGC CAC AAC TTT ACC CAG GAG TGC AAC TGT TCC ATC 351
 25 TAC CAA GGT CAT ATC ACC GGC CAC CGC ATG GCA TGG GAC 390
 ATG ATG CTA AAC TGG TCA CCA ACT CTT ACC ATG ATC CTC 429
 GCC TAT GCC GCT CGT GTT CCT GAG CTA GCC CTC CAG GTT 468
 GTC TTC GGC GGC CAT TGG GGC GTG GTT GGC TTG GCC 507
 TAT TTC TCC ATG CAG GGA GCG TGG GCC AAA GTC ATT GCC 546
 ATC CTC CTT CTT GTC GCA GGA GTG GAT GCA 576

30 (2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

5	GTG	GAA	GTC	AGG	AAC	ACC	AGT	TCT	AGT	TAC	TAC	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AAC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
	AAT	GAC	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCA	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAT	ATA	GAT	ATG	ATT	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	GTG	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	GTA	TCG	CCA	312
10	GAA	CAC	CAC	CAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CAC	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
	ATG	ATG	CTT	AAC	TGG	TCA	CCA	ACT	CTC	ACC	ATG	ATC	CTC	429
	GCC	TAT	GCC	GCC	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTC	468
	GTC	TTC	GGT	GGT	CAT	TGG	GGT	GTG	TTT	GGC	TTG	GCC	GCC	507
	TAT	TTC	TCC	ATG	CAG	GGA	GCG	TGG	GCC	AAG	GTC	ATT	GCC	546
	ATC	CTC	CTT	CTT	GTA	GCA	GGA	GTG	GAT	GCA				576

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

25	GTG	GAA	GTC	AGG	AAC	ATC	AGT	TCT	AGC	TAC	TAT	GCC	ACC	39
	AAT	GAT	TGC	TCA	AAC	AGC	AGC	ATC	ACC	TGG	CAA	CTC	ACC	78
	AAC	GCA	GTC	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CGG	TGT	GAG	117
	AAT	GAT	AAT	GGC	ACC	CTG	CAC	TGC	TGG	ATA	CAA	GTG	ACA	156
	CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGC	GGC	GCG	CTC	ACT	CAC	195
	AAC	CTG	CGA	GCA	CAC	GTC	GAT	ATG	ATC	GTA	ATG	GCA	GCT	234
	ACG	GTC	TGC	TCG	GCC	TTG	TAT	GTG	GGA	GAC	ATG	TGC	GGG	273
	GCC	GTG	ATG	ATC	GTG	TCG	CAG	GCT	TTC	ATA	ATA	TCG	CCA	312
30	GAA	GCG	CAC	AAC	TTT	ACC	CAA	GAG	TGC	AAC	TGT	TCC	ATC	351
	TAC	CAA	GGT	CGT	ATC	ACC	GGC	CAC	CGC	ATG	GCG	TGG	GAC	390
	ATG	ATG	CTA	AAC	TGG	TCA	CCA	ACT	CTT	ACC	ATG	ATC	CTT	429
	GCC	TAT	GCC	GCT	CGT	GTT	CCT	GAG	CTA	GTC	CTT	GAA	GTT	468
	GTC	TTC	GCG	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
	TAT	TTC	TCC	ATG	CAA	GGA	GCG	TGG	GCC	AAG	GTC	ATT	GCC	546
	ATC	CTC	CTG	CTT	GTC	GCA	GGA	GTG	GAT	GCA				576

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTG	GAA	GTT	AGA	AAC	ACC	AGT	TTT	AGC	TAC	TAC	GCC	ACC	39
AAT	GAT	TGC	TCG	AAC	AAC	AGC	ATC	ACC	TGG	CAG	CTC	ACC	78
AAC	GCA	GTT	CTC	CAC	CTT	CCC	GGA	TGC	GTC	CCA	TGT	GAG	117
AAT	GAC	AAT	GGC	ACC	TTG	CGC	TGC	TGG	ATA	CAA	GTA	ACA	156
CCT	AAT	GTG	GCT	GTG	AAA	CAC	CGT	GGC	GCA	CTC	ACT	CAC	195
AAC	CTG	CGA	ACG	CAT	GTC	GAC	GTG	ATC	GTA	ATG	GCA	GCT	234
ACG	GTG	TGC	TCG	GCC	TTG	TAT	GTG	GGG	GAC	GTG	TGC	GGG	273
GCC	GTG	ATG	ATA	GCG	TCG	CAG	GCT	TTC	ATA	ATA	TCG	CCA	312
GAA	CGC	CAC	AAC	TTC	ACC	CAG	GAG	TGC	AAC	TGT	TCC	ATC	351
TAC	CAA	GGT	CAT	ATC	ACC	GGC	CAC	CGC	ATG	GCA	TGG	GAC	390
ATG	ATG	CTG	AAC	TGG	TCA	CCA	ACT	CTC	ACC	ATG	ATC	CTC	429
GCC	TAC	GCT	GCT	CGT	GTG	CCT	GAA	CTA	GTC	CTT	GAA	GTT	468
GTC	TTC	GGC	GGC	CAT	TGG	GGC	GTG	GTG	TTT	GGC	TTG	GCC	507
TAT	TTC	TCC	ATG	CAA	GGA	GCG	TGG	GCC	AAA	GTC	ATC	GCC	546
ATC	CTC	CTC	CTT	GTC	GCA	GGA	GTG	GAC	GCA				576

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GTG	GAG	GTC	AAG	GAC	ACC	GGC	GAC	TCC	TAC	ATG	CCG	ACC	39
AAC	GAT	TGC	TCC	AAC	TCT	AGT	ATC	GTT	TGG	CAG	CTT	GAA	78
GGA	GCA	GTG	CTT	CAT	ACT	CCT	GGA	TGC	GTC	CCT	TGT	GAG	117
CGT	ACC	GCC	AAC	GTC	TCT	CGA	TGT	TGG	GTG	CCG	GTT	GCC	156
CCC	AAT	CTC	GCC	ATA	AGT	CAA	CCT	GGC	GCT	CTC	ACT	AAG	195

0

	GGC	CTG	CGA	GCA	CAC	ATC	GAT	ATC	ATC	GTG	ATG	TCT	GCT	234
	ACG	GTC	TGT	TCT	GCC	CTT	TAT	GTG	GGG	GAC	GTG	TGT	GGC	273
	GCG	CTG	ATG	CTG	GCC	GCT	CAG	GTC	GTC	GTC	GTG	TCG	CCA	312
	CAA	CAC	CAT	ACG	TTT	GTC	CAG	GAA	TGC	AAC	TGT	TCC	ATA	351
	TAC	CCG	GGC	CGC	ATT	ACG	GGA	CAC	CGC	ATG	GCT	TGG	GAT	390
	ATG	ATG	ATG	AAC	TGG	TCG	CCC	ACT	ACC	ACC	ATG	CTC	CTG	429
5	GCG	TAC	TTG	GTG	CGC	ATC	CCG	GAA	GTC	ATC	TTG	GAT	ATT	468
	GTT	ACA	GGA	GGT	CAT	TGG	GGT	GTA	ATG	TTT	GGC	CTC	GCT	507
	TAC	TTC	TCC	ATG	CAG	GGA	TCG	TGG	GCG	AAG	GTC	ATC	GTT	546
	ATC	CTC	CTG	CTG	ACT	GCT	GGG	GTG	GAG	GCG				576

(2) INFORMATION FOR SEQ ID NO:35:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK12

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

20 TTA GAG TGG CGG AAT GTG TCC GGC CTC TAC GTC CTT ACC 39
 AAC GAC TGT TCC AAT AGC AGT ATC GTG TAT GAG GCC GAT 78
 GAC GTC ATT CTG CAC ACA CCT GGC TGT GTA CCT TGT GTT 117
 CAG GAC GGC AAT ACA TCT ACG TGC TGG ACC TCA GTG ACG 156
 CCT ACA GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT 195
 TCG ATA CGC AGT CAT GTG GAC CTG CTA GTG GGC GCG GCC 234
 ACG ATG TGC TCT GCG CTC TAC GTG GGT GAT GTG TGT GGG 273
 GCC GTC TTC CTT GTG GGA CAA GCC TTC ACG TTC AGA CCT 312
 CGT CGC CAT CAA ACA GTC CAG ACC TGT AAC TGC TCG CTG 351
 TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT 390
 ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTA 429
 25 GCG CAC GTC CTG CGT CTG CCC CAG ACC TTG TTC GAC ATA 468
 ATA GCT GGG GCC CAT TGG GGC ATC ATG GCG GGC CTA GCC 507
 TAT TAC TCC ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546
 ATC ATG GTT ATG TTT TCA GGA GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:36:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

35

(C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

	CTA	GAG	TGG	CGG	AAT	GTG	TCT	GGC	CTC	TAT	GTC	CTT	ACC	39
	AAC	GAC	TGT	CCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
5	GAC	GTC	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGC	AAT	ACA	TCC	ACG	TGC	TGG	ACC	TCG	GTG	ACA	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAC	GTC	GGA	GCA	ACC	ACC	GCC	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTG	TTA	GTG	GGC	GCG	GCC	234
	ACG	ATG	TGC	TCT	GCG	CTC	TAC	GTG	GGC	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTC	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCG	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
	TAC	CCA	GGC	CAC	CTT	TCA	GGA	CAT	CGA	ATG	GCT	TGG	GAT	390
10	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCC	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	GTC	CTG	CGG	TTG	CCC	CAG	ACC	TTG	TTC	GAC	ATA	468
	ATA	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCA	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAG	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGG	GTC	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:37:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: hom sapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

	CTA	GAG	TGG	CGG	AAT	ACG	TCT	GGC	CTC	TAT	GTC	CTC	ACC	39
	AAC	GAC	TGT	TCC	AAT	AGC	AGT	ATT	GTG	TAT	GAG	GCC	GAT	78
25	GAC	GTT	ATT	CTG	CAC	ACA	CCT	GGC	TGT	GTA	CCT	TGT	GTT	117
	CAG	GAC	GGT	AAT	ACA	TCC	ACG	TGC	TGG	ACC	CCA	GTG	ACA	156
	CCT	ACA	GTG	GCA	GTC	AGG	TAT	GTC	GGA	GCA	ACC	ACC	GCT	195
	TCG	ATA	CGC	AGT	CAT	GTG	GAC	CTA	TTG	GTG	GGC	GCG	GCC	234
	ACT	ATG	TGC	TCT	GGG	CTC	TAC	GTG	GGT	GAT	ATG	TGT	GGG	273
	GCC	GTC	TTT	CTC	GTG	GGA	CAA	GCC	TTC	ACG	TTC	AGA	CCT	312
	CGT	CGC	CAT	CAA	ACG	GTC	CAG	ACC	TGT	AAC	TGC	TCG	CTG	351
	TAC	CCA	GGC	CAT	CTT	TCA	GGA	CAT	CGC	ATG	GCT	TGG	GAT	390
30	ATG	ATG	ATG	AAT	TGG	TCC	CCC	GCT	GTG	GGT	ATG	GTG	GTG	429
	GCG	CAC	GTT	CTG	CGT	TTG	CCC	CAG	ACC	GTG	TTC	GAC	ATA	468
	ATA	GCC	GGG	GCC	CAT	TGG	GGC	ATC	TTG	GCG	GGC	CTA	GCC	507
	TAT	TAC	TCC	ATG	CAA	GGC	AAC	TGG	GCC	AAG	GTC	GCT	ATC	546
	ATC	ATG	GTT	ATG	TTT	TCA	GGG	GTC	GAC	GCC				576

35

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

10	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT GTC CTT ACC	39
	AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT	78
	GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT	117
	CAG GAC GGC AAT ACA TCC ATG TGC TGG ACC CCA GTG ACA	156
	CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT	195
	TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC	234
	ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG	273
	GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT	312
15	CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG	351
	TAC CCA GGC CAT GTT TCA GGA CAT CGA ATG GCT TGG GAT	390
	ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG	429
	GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA	468
	CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC	507
	TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATT	546
	GTC ATG ATT ATG TTT TCA GGG GTC GAT GCC	576

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

30	CTA GAG TGG CGG AAT ACG TCT GGC CTC TAT ATC CTT ACC	39
	AAC GAC TGT TCC AAT AGC AGT ATT GTG TAT GAG GCC GAT	78
	GAC GTC ATT CTG CAC ACA CCC GGC TGT GTA CCT TGT GTT	117
	CAG GAC GGC AAT ACA TCC ACG TGC TGG ACC CCA GTG ACA	156
	CCT ACG GTG GCA GTC AGG TAC GTC GGA GCA ACC ACC GCT	195
	TCG ATA CGC AGT CAT GTG GAC CTA TTA GTG GGC GCG GCC	234
	ACG CTG TGC TCT GCG CTC TAT GTG GGT GAT ATG TGT GGG	273

5
 GCC GTC TTT CTC GTG GGA CAA GCC TTC ACG TTC AGA CCT 312
 CGT CGC CAT CAA ACG GTC CAG ACC TGT AAC TGC TCG CTG 351
 TAC CCA GGC CAT CTT TCA GGA CAT CGA ATG GCT TGG GAT 390
 ATG ATG ATG AAT TGG TCC CCC GCT GTG GGT ATG GTG GTG 429
 GCG CAC ATC CTG CGA TTG CCC CAG ACC TTG TTT GAC ATA 468
 CTG GCC GGG GCC CAT TGG GGC ATC TTG GCG GGC CTA GCC 507
 TAT TAT TCT ATG CAG GGC AAC TGG GCC AAG GTC GCT ATC 546
 ATC ATG ATT ATG TTT TCA GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:40:

10
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z4

15
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

20
 GAG CAC TAC CGG AAT GCT TCG GGC ATC TAT CAC ATC ACC 39
 AAT GAT TGT CCG AAT TCC AGT ATA GTC TAT GAA GCT GAC 78
 CAT CAC ATC CTA CAC TTG CCG GGG TGC GTA CCC TGT GTG 117
 ATG ACT GGG AAC ACA TCG CGT TGC TGG ACG CCG GTG ACG 156
 CCT ACA GTG GCT GTC GCA CAC CCG GGC GCT CCG CTT GAG 195
 TCG TTC CGG CGA CAT GTG GAC TTA ATG GTA GGC GCG GCC 234
 ACT TTG TGT TCT GCC CTC TAT GTT GGG GAC CTC TGC GGA 273
 GGT GCC TTC CTG ATG GGG CAG ATG ATC ACT TTT CCG CCG 312
 CGT CGC CAC TGG ACC ACG CAG GAG TGC AAT TGT TCC ATC 351
 TAC ACT GGC CAT ATC ACC GGC CAC AGG ATG GCG TGG GAC 390
 ATG ATG ATG AAC TGG AGC CCT ACC ACC ACT CTG CTC CTC 429
 GCC CAG ATC ATG AGG GTC CCC ACA GCC TTT CTC GAC ATG 468
 GTT GCC GGA GGC CAA TGG GGC GTC CTC GCG GGC TTG GCG 507
 25 TAC TTC AGC ATG CAA GGC AAT TGG GCC AAG GTA GTC CTG 546
 GTC CTT CTC CTC TTT GCT GGG GTA GAC GCC 576

(2) INFORMATION FOR SEQ ID NO:41:

30
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z1

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

	GTG	CAC	TAC	CGG	AAT	GCT	TCG	GGC	GTC	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCT	AAC	ACC	AGC	ATA	GTG	TAC	GAG	ACG	GAG	78
	CAC	CAC	ATC	ATG	CAC	TTG	CCA	GGG	TGT	GTC	CCC	TGT	GTG	117
	CGG	ACG	GAG	AAT	ACT	TCT	CGC	TGC	TGG	GTG	CCC	TTG	ACC	156
	CCC	ACT	GTG	GCC	CGC	CCC	TAT	CCC	AAC	GCA	CCG	TTA	GAG	195
5	TCC	ATG	CGC	AGG	CAT	GTA	GAC	CTG	ATG	GTG	GGT	GCG	GCT	234
	ACT	ATG	TGT	TCC	GCC	TTC	TAC	ATT	GGA	GAT	CTG	TGT	GGA	273
	GGC	GTC	TTC	CTA	GTG	GGC	CAG	CTG	TTC	GAC	TTC	CGA	CCG	312
	CGC	CGG	CAC	TGG	ACC	ACC	CAG	GAT	TGC	AAC	TGC	TCC	ATC	351
	TAT	CCT	GGT	CAC	GTC	TCG	GGC	CAC	AGG	ATG	GCC	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGC	CCT	ACC	AGC	GCG	CTG	ATT	ATG	429
	GCT	CAG	ATC	TTA	CGG	ATC	CCC	TCT	ATC	CTA	GGT	GAC	TTG	468
10	CTC	ACC	GGG	GGT	CAC	TGG	GGA	GTT	CTT	GCT	GGT	CTA	GCT	507
	TTC	TTC	AGC	ATG	CAG	AGT	AAC	TGG	GCG	AAG	GTC	ATC	CTG	546
	GTC	CTA	TTC	CTC	TTT	GCC	GGG	GTC	GAG	GGA				576

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: hom sapiens
 (C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

	GTT	AAC	TAT	CGC	AAT	GCC	TCG	GGC	GTC	TAT	CAC	GTC	ACC	39
	AAC	GAC	TGC	CCG	AAC	TCG	AGC	ATA	GTG	TAT	GAG	GCC	GAA	78
	CAC	CAG	ATC	TTA	CAC	CTC	CCA	GGG	TGC	TTG	CCC	TGT	GTG	117
	AGG	GTT	GGG	AAT	CAG	TCA	CGC	TGC	TGG	GTG	GCC	CTT	ACT	156
	CCC	ACC	GTG	GCG	GTG	TCT	TAT	ATC	GGT	GCT	CCG	CTT	GAC	195
25	TCC	CTC	CGG	AGA	CAT	GTG	GAC	CTG	ATG	GTG	GGC	GCC	GCT	234
	ACT	GTA	TGC	TCT	GCC	CTC	TAC	GTT	GGA	GAT	CTG	TGC	GGT	273
	GGT	GCA	TTT	TTG	GTT	GGC	CAG	ATG	TTC	TCC	TTC	CAG	CCG	312
	CGA	CGC	CAC	TGG	ACT	ACG	CAG	GAC	TGC	AAT	TGT	TCT	ATC	351
	TAC	GCA	GGG	CAT	ATC	ACG	GGC	CAC	AGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAC	TGG	AGT	CCC	ACA	ACC	ACC	CTG	CTT	CTC	429
	GCC	CAG	GTC	ATG	AGG	ATC	CCT	AGC	ACT	CTG	GTA	GAT	CTA	468
30	CTC	GCT	GGA	GGG	CAC	TGG	GGC	GTC	CTT	GTT	GGG	TTG	GCG	507
	TAC	TTC	AGT	ATG	CAT	GCT	AAT	TGG	GCC	AAA	GTC	ATC	CTG	546
	GTC	CTT	TTC	CTC	TTC	GCT	GGA	GTT	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:43:

35

°
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

	GTC AAC TAT CAC AAT GCC TCG GGC GTC TAT CAC ATC ACC	39
	AAC GAC TGC CCG AAC TCG AGC ATA ATG TAT GAG GCC GAA	78
10	CAC CAC ATC CTA CAC CTC CCA GGG TGC GTA CCC TGT GTG	117
	AGG GAG GGG AAC CAG TCA CGC TGC TGG GTG GCC CTT ACT	156
	CCC ACC GTG GCG GCG CCT TAT ATC GGT GCA CCG CTT GAA	195
	TCC ATC CGG AGA CAT GTG GAC CTG ATG GTA GGC GCT GCT	234
	ACA GTG TGC TCC GCT CTC TAC ATT GGG GAC CTG TGC GGT	273
	GGC GTA TTT TTG GTT GGT CAG ATG TTT TCT TTC CAG CCG	312
	CGA CGC CAC TGG ACT ACG CAG GAC TGC AAT TGT TCC ATC	351
15	TAT GCG GGG CAC GTT ACA GGC CAC AGA ATG GCA TGG GAC	390
	ATG ATG ATG AAC TGG AGT CCC ACA ACC ACC TTG GTC CTC	429
	GCC CAG GTT ATG AGG ATC CCT AGC ACT CTG GTG GAC CTA	468
	CTC ACT GGA GGG CAC TGG GGT ATC CTT ATC GGG GTG GCA	507
	TAC TTC TGC ATG CAA GCT AAT TGG GCC AAG GTC ATT CTG	546
	GTC CTT TTC CTC TAC GCT GGA GTT GAT GCC	576

20 (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

	TAC AAC TAT CGC AAC AGC TCG GGT GTC TAC CAT GTC ACC	39
	AAC GAT TGC CCG AAC TCG AGC ATA GTC TAT GAA ACC GAT	78
30	TAC CAC ATC TTA CAC CTC CCG GGA TGC GTT CCT TGC GTG	117
	AGG GAA GGG AAC AAG TCT ACA TGC TGG GTG TCT CTC ACC	156
	CCC ACC GTG GCT GCG CAA CAT CTG AAT GCT CCG CTT GAG	195
	TCT TTG AGA CGT CAC GTG GAT CTG ATG GTG GGC GGC GCC	234
	ACT CTC TGC TCC GCC CTC TAC ATC GGA GAC GTG TGT GGG	273
	GGT GTG TTC TTG GTC GGT CAA CTG TTC ACC TTC CAA CCT	312
35	CGC CGC CAC TGG ACC ACC CAA GAC TGC AAT TGT TCC ATC	351

TAC ACA GGA CAT ATC ACA GGA CAC AGA ATG GCT TGG GAC 390
 ATG ATG ATG AAT TGG AGC CCC ACT GCG ACG CTG GTC CTC 429
 GCC CAA CTT ATG AGG ATC CCA GGC ATG GTC GAC CTG 468
 CTT GCA GGC GGC CAC TGG GGC ATT CTG GTT GGC ATA GCG 507
 TAC TTC AGC ATG CAA GCT AAT TGG GCC AAG GTT ATC CTG 546
 GTC CTG TTT CTC TTT GCT GGA GTC GAC GCT 576

5

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

15 GTT CCC TAC CGG AAT GCC TCT GGG GTT TAC CAT GTC ACC 39
 AAT GAC TGC CCA AAC TCC TCC ATA GTC TAC GAG GCT GAT 78
 AGC CTG ATC TTG CAC GCA CCT GGC TGC GTG CCC TGT GTC 117
 AGG CAA GAT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC 156
 CCC ACA CTG TCA GCC CCG ACC TTC GGA GCG GTC ACG GCT 195
 CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGA GGA GCT 234
 GCT CTC TGC TCC GCA CTA TAC GTC GGC GAC GCG TGC GGG 273
 20 GCA GTG TTT CTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312
 CGC CAG CAT ACC ACA GTG CAG GAC TGC AAC TGT TCC ATT 351
 TAC AGT GGC CAT ATC ACC GGC CAC CGG ATG GCT TGG GAC 390
 ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG CTG ATG 429
 GCC CAG ATG CTA GGC ATC CCC CAG GTG GTC ATA GAC ATC 468
 ATA GCC GGG GGC CAC TGG GGG GTC TTG TTT GCC GCC GCA 507
 TAC TTT GCG TCG GCC GCC AAC TGG GCT AAG GTA GTG CTG 546
 GTT CTG TTC CTG TTT GCG GGG GTC GAT GGC 576

25

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

35

0
 GTT CCC TAC CGA AAC GCC TCT GGG GTT TAT CAT GTC ACC 39
 AAT GAT TGC CCA AAC TCT TCC ATA GTT TAC GAG GCT GAT 78
 AAC CTG ATC TTG CAT GCA CCT GGT TGC GTG CCT TGT GTC 117
 AGG CAA GAT AAT GTC AGT AAG TGC TGG GTC CAA ATC ACC 156
 CCC ACG TTG TCA GCC CCG AAT CTC GGA GCG GTC ACG GCT 195
 CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGA GGG GCT 234
 5 GCC CTC TGC TCC GCA CTA TAC GTC GGG GAC GCG TGC GGG 273
 GCA GTG TTT TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312
 CGC CAG CAC ACT ACG GTG CAA GAC TGC AAT TGC TCT ATT 351
 TAC AGT GGC CAT ATC ACC GGC CAC CGG ATG GCA TGG GAC 390
 ATG ATG ATG AAT TGG TCA CCT ACG ACG GCC TTG CTG ATG 429
 GCC CAG TTG CTA CGG ATT CCC CAG GTG GTC ATC GAC ATC 468
 ATT GCC GGG GGC CAC TGG GGG GTC TTG TTT GCC GCC GCA 507
 TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT ATA CTG 546
 10 GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

20 GTC CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC ACC 39
 AAT GAT TGC CCA AAC TCT TCC ATA GTC TAC GAG GCT GAT 78
 AAC CTG ATT CTG CAC GCA CCT GGT TGC GTG CCC TGT GTC 117
 AAG GAA GGT AAT GTC AGT AGG TGC TGG GTC CAA ATC ACC 156
 CCC ACA TTG TCA GCC CCG AAC CTC GGA GCG GTC ACG GCT 195
 CCT CTT CGG AGG GTC GTT GAC TAC TTA GCG GGA GGG GCT 234
 25 GCC CTC TGC TCC GCA CTA TAC GTC GGG GAC GCG TGC GGG 273
 GCA GTG TTC TTG GTA GGC CAA ATG TTC ACC TAT AGG CCT 312
 CGC CAG CAT ACT ACG GTG CAG GAC TGC AAC TGT TCC ATT 351
 TAC AGC GGC CAT ATC ACC GGC CAC CGA ATG GCA TGG GAC 390
 ATG ATG ATG AAT TGG TCA CCT ACG ACA GCC TTG GTG ATG 429
 GCC CAG GTG CTA CGG ATT CCC CAA GTG GTC ATT GAC ATC 468
 ATT GCC GGG GGC CAC TGG GGG GTC TTG TTC GCC GTC GCA 507
 TAC TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG 546
 30 GTC CTG TTT CTG TTT GCG GGG GTC GAT GGC 576

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 576 base pairs
 (B) TYPE: nucleic acid

o

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA6

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

	GTT	CCT	TAC	CGG	AAT	GCC	TCT	GGG	GTG	TAT	CAT	GTT	ACC	39
	AAT	GAT	TGC	CCA	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCT	GAT	78
	GAC	CTG	ATC	CTA	CAC	GCA	CCT	GGC	TGC	GTG	CCC	TGT	GTC	117
	CGG	AAG	GAT	AAT	GTC	AGT	AGA	TGC	TGG	GTT	CAT	ATC	ACC	156
	CCC	ACA	CTA	TCA	GCC	CCG	AGC	CTC	GGA	GCG	GTC	ACG	GCT	195
10	CCT	CTT	CGG	AGG	GCC	GTT	GAT	TAC	TTG	GCG	GGA	GGG	GCC	234
	GCC	CTG	TGC	TCC	GCG	TTA	TAC	GTC	GGA	GAC	GTG	TGC	GGG	273
	GCA	TTG	TTT	TTG	GTA	GGC	CAA	ATG	TTC	ACC	TAT	AGG	CCT	312
	CGC	CAG	CAT	GCT	ACG	GTA	CAG	GAC	TGC	AAC	TGC	TCC	ATT	351
	TAC	AGT	GGC	CAT	ATC	ACT	GGC	CAC	CGG	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCC	GCG	ACA	GCC	TTG	GTG	ATG	429
	GCC	CAA	ATG	CTA	CGG	ATT	CCC	CAG	GTG	GTC	ATT	GAC	ATC	468
	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GCT	GCA	507
15	TAC	TTC	GCG	TGC	GCG	GCT	AAC	TGG	GCT	AAG	GTT	GTG	CTG	546
	GTC	TTG	TTT	CTG	TTT	GCG	GGG	GTT	GAT	GCC				576

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA7

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

	GTC	CCC	TAC	CGA	AAT	GCC	TCC	GGG	GTT	TAT	CAT	GTC	ACC	39
	AAT	GAT	TGC	CCG	AAC	TCT	TCC	ATA	GTC	TAT	GAG	GCT	GAC	78
	AAC	CTG	ATC	CTG	CAC	GCA	CCT	GGT	TGC	GTG	CCC	TGT	GTC	117
	AGA	CAA	AAT	AAT	GTC	AGT	AGG	TGC	TGG	GTC	CAA	ATC	ACC	156
	CCC	ACA	TTG	TCA	GCC	CCG	AAC	CTC	GGA	GCG	GTC	ACG	GCT	195
	CCT	CTT	CGG	AGG	GCC	GTT	GAC	TAC	CTA	GCG	GGA	GGG	GCT	234
30	GCC	CTC	TGC	TCC	GCG	CTA	TAC	GTC	GGG	GAC	GCG	TGC	GGG	273
	GCA	GTG	TTT	TTG	GTA	GGC	CAG	ATG	TTC	AGC	TAT	AGG	CCT	312
	CGC	CAG	CAC	ACT	ACG	GTG	CAG	GAC	TGC	AAC	TGT	TCC	ATT	351
	TAC	AGT	GGC	CAT	ATC	ACC	GGC	CAC	CGA	ATG	GCA	TGG	GAC	390
	ATG	ATG	ATG	AAT	TGG	TCA	CCT	ACG	ACA	GCC	TTG	GTG	ATG	429
	GCC	CAG	TTG	CTA	CGG	ATT	CCC	CAG	GTG	GTC	ATC	GAC	ATC	468
35	ATT	GCC	GGG	GGC	CAC	TGG	GGG	GTC	TTG	TTC	GCC	GCC	GCA	507

TAT TTC GCG TCA GCG GCT AAC TGG GCT AAG GTT GTG CTG 546
GTC TTG TTT CTG TTT GCG GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GTT CCC TAC CGA AAT GCC TCT GGG GTT TAT CAT GTC ACC 39
AAT GAT TGC CCA AAC TCT TCC ATC GTC TAC GAG GCT GAT 78
GAC CTG ATC TTA CAC GCA CCT GGT TGC GTG CCC TGT GTT 117
AGG CAG GGT AAT GTC AGT AGG TGC TGG GTC CAG ATC ACC 156
CCC ACA CTG TCA GCC CCG AGC CTC GGA GCG GTC ACG GCT 195
CCT CTT CGG AGG GCC GTT GAC TAC TTA GCG GGG GGG GCT 234
GCC CTT TGC TCC GCG TTA TAC GTC GGA GAC GCG TGC GGG 273
GCA GTG TTT TTG GTA GGT CAA ATG TTC ACC TAT AGC CCT 312
CGC CGG CAT AAT GTT GTG CAG GAC TGC AAC TGT TCC ATT 351
TAC AGT GGC CAC ATC ACC GGC CAC CGG ATG GCA TGG GAC 390
ATG ATG ATG AAT TGG TCA CCT ACA ACA GCT TTG GTG ATG 429
GCC CAG TTG TTA CGG ATT CCC CAG GTG GTC ATT GAC ATC 468
ATT GCC GGG GCC CAC TGG GGG GTC TTG TTC GCC GCC GCA 507
TAC TAC GCG TCG GCG GCT AAC TGG GCC AAG GTT GTG CTG 546
GTC CTG TTT CTG TTT GCG GGG GTC GAT GCC 576

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 576 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CTT ACC TAC GGC AAC TCC AGT GGG CTA TAC CAT CTC ACA 39
AAT GAT TGC CCC AAC TCC AGC ATC GTG CTG GAG GCG GAT 78
GCT ATG ATC TTG CAT TTG CCT GGA TGC TTG CCT TGT GTG 117
AGG GTC GAT GAT CGG TCC ACC TGT TGG CAT GCT GTG ACC 156

0
 CCC ACC CTG GCC ATA CCA AAT GCT TCC ACG CCC GCA ACG 195
 GGA TTC CGC AGG CAT GTG GAT CTT CTT GCG GGC GCC GCA 234
 GTG GTT TGC TCA TCC CTG TAC ATC GGG GAC CTG TGT GGC 273
 TCT CTC TTT TTG GCG GGA CAA CTA TTC ACC TTT CAG CCC 312
 CGC CGT CAT TGG ACT GTG CAA GAC TGC AAC TGC TCC ATC 351
 TAT ACA GGC CAC GTC ACC GGC CAC AGG ATG GCT TGG GAC 390
 5 ATG ATG ATG AAC TGG TCA CCC ACA ACC ACT CTG GTC CTA 429
 TCT AGC ATC TTG AGG GTA CCT GAG ATT TGT GCG AGT GTG 468
 ATA TTT GGT GGC CAT TGG GGG ATA CTA CTA GCC GTT GCC 507
 TAC TTT GGC ATG GCT GGC AAC TGG CTA AAA GTT CTG GCT 546
 GTT CTG TTC CTA TTT GCA GGG GTT GAA GCA 576

(2) INFORMATION FOR SEQ ID NO:52:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
 5 10 15
 20 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Val Ser
 35 40 45
 Arg Cys Trp Val Ala Met Thr Pro Thr Val Ala Thr Arg Asp Gly
 50 55 60
 Lys Leu Pro Thr Ala Gln Leu Arg Arg His Ile Asp Leu Leu Val
 65 70 75
 25 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Gly Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 30 Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180

° Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK9

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

	Tyr	Gln	Val	Arg	Asn	Ser	Ser	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
15	His	Ser	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	
					35					40					45	
	Lys	Cys	Trp	Val	Ala	Val	Ala	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
20	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
25					140					145					150	
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Val	Val	Val	Leu	Leu	Leu	Phe	Thr	Gly	Val	Asp	Ala				
					185					190						

30

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DR1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

5 His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Ala Ile Leu
30
His Ala Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
45
10 Arg Cys Trp Val Ala Val Thr Pro Thr Val Ala Thr Arg Asp Gly
60
Lys Leu Pro Thr Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
90
Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
105
15 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
135
Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
150
Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
165
20 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
180
Val Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
190

(2) INFORMATION FOR SEQ ID NO:55:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

30 (C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

His Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
5 10 15

35

°	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Thr	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Ala	Val	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	
5	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
	His	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
10	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala				
15					185					190						

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Thr	Ser	
					35					40					45	
30	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Ala	Thr	Gln	Leu	Arg	Arg	Tyr	Ile	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	

```

° Gly Ser Val Phe Leu Val Gly Gln Leu Phe Thr Phe Ser Pro Arg
  95 100 105
Arg Leu Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
  110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
  125 130 135
Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
  140 145 150
5 Gln Ala Ile Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
  155 160 165
Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
  170 175 180
Leu Val Val Leu Leu Leu Phe Ala Gly Val Asp Ala
  185 190

```

10

(2) INFORMATION FOR SEQ ID NO:57:

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 192 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: unknown
    (D) TOPOLOGY: unknown

```

15

```

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: homosapiens
    (C) INDIVIDUAL ISOLATE: S18

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

20 Tyr Gln Val Arg Asn Ser Thr Gly Leu Tyr His Val Thr Asn Asp
   5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Thr Ile Leu
  20 25 30
His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ala Ser
  35 40 45
Arg Cys Trp Val Pro Val Ala Pro Thr Val Ala Thr Arg Asp Gly
  50 55 60
25 Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
   65 70 75
Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
   80 85 90
Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Ile Ser Pro Arg
   95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
  110 115 120
30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
  125 130 135
Ser Pro Thr Thr Ala Leu Val Ile Ala Gln Leu Leu Arg Val Pro
  140 145 150
Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
  155 160 165

```

35

° Ala Gly Ile Ala Tyr Phe Ser Met Ala Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Leu Val Leu Leu Leu Phe Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:58:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 10 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Tyr Gln Val Arg Asn Ser Ser Gly Leu Tyr His Val Thr Asn Asp
 5 10 15
 Cys Pro Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Ala Ile Leu
 15 20 25 30
 His Ser Pro Gly Cys Val Pro Cys Val Arg Glu Asp Gly Ala Pro
 35 40 45
 Lys Cys Trp Val Ala Val Ala Pro Thr Val Ala Thr Arg Asp Gly
 50 55 60
 Lys Leu Pro Ala Thr Gln Leu Arg Arg His Ile Asp Leu Leu Val
 65 70 75
 20 Gly Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 25 Ser Pro Thr Thr Ala Leu Val Val Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Leu Asp Met Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Ile Ala Tyr Phe Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Leu Leu Leu Phe Ser Gly Val Asp Ala
 185 190
 30

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid

o

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US11

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

	Tyr	Gln	Val	Arg	Asn	Ser	Thr	Gly	Leu	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Ala	Ile	Leu	
					20					25					30	
10	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ala	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Ala	Met	Thr	Pro	Thr	Val	Ala	Thr	Arg	Asp	Gly	
					50					55					60	
	Lys	Leu	Pro	Thr	Thr	Gln	Leu	Arg	Arg	His	Ile	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Ser	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
15					95					100					105	
	Arg	His	Trp	Thr	Thr	Gln	Gly	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
20	Gln	Ala	Ile	Leu	Asp	Met	Ile	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Leu	Val	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

25

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

35

°	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Gly
					50					55					60
5	Asn	Val	Pro	Thr	Thr	Ala	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Ile	Ser	Gln	Leu	Phe	Thr	Leu	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
10	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Met	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
15	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: D3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	Gln	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
30	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asp	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser
					50					55					60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75


```

°   Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
    80                      85                      90
    Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
    95                      100                     105
    Arg His Glu Thr Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
    110                     115                     120
    His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                     130                     135
5   Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
    140                     145                     150
    Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
    155                     160                     165
    Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
    170                     175                     180
    Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
    185                     190
10

```

(2) INFORMATION FOR SEQ ID NO:62:

```

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 192 amino acids
        (B) TYPE: amino acid
15      (C) STRANDEDNESS: unknown
        (D) TOPOLOGY: unknown

```

```

    (vi) ORIGINAL SOURCE:
        (A) ORGANISM: hom sapiens
        (C) INDIVIDUAL ISOLATE: DK1

```

```

20      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

    Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
        5                      10                      15
    Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Val Asp Val Ile Met
        20                      25                      30
    His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn His Ser
        35                      40                      45
25   Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
        50                      55                      60
    Ser Ile Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
        65                      70                      75
    Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
        80                      85                      90
    Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
        95                      100                     105
30   Arg His Glu Thr Ala Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
        110                     115                     120
    His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
        125                     130                     135
    Ser Pro Thr Thr Ala Leu Val Leu Ser Gln Leu Leu Arg Ile Pro
        140                     145                     150

```

° Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Ala Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
 185 190

5 (2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

15 Tyr Glu Val Arg Asn Val Ser Gly Ile Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Val Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Val
 50 55 60
 20 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Leu Tyr Pro Gly
 110 115 120
 25 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 30 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

	His	Glu	Val	His	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	
10					20					25						30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	
					35					40						45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	
					50					55						60
	Ser	Ile	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70						75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	
15					80					85						90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100						105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115						120
	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
20	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Leu	Pro	
					140					145						150
	Gln	Ala	Val	Met	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160						165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175						180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				
25					185					190						

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

o

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Leu	Ser	Ile	Val	Tyr	Glu	Thr	Thr	Asp	Met	Ile	Met	
					20					25						30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	
					35					40						45
5	Arg	Cys	Trp	Val	Ala	Leu	Ala	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	
					50					55						60
	Ser	Val	Pro	Thr	Thr	Ala	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70						75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85						90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100						105
10	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115						120
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145						150
15	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160						165
	Ala	Gly	Leu	Ala	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val		170
					175					180						185
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				190
					185					190						

(2) INFORMATION FOR SEQ ID NO:66:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ile	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met	
					20					25						30
	His	Thr	Pro	Gly	Cys	Met	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	
					35					40						45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Val	
					50					55						60
	Ser	Val	Pro	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val		65
					65					70						75

35

Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 5 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 10 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
 50 55 60
 Ser Val Ser Thr Thr Thr Ile Arg His His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 30 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150

o

Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
				155					160					165
Ala	Gly	Leu	Ala	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
				170					175					180
Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
				185					190					

5

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

15	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Phe	Ser
					35					40					45
	Ser	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
					50					55					60
20	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
25	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
					155					160					165
30	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:69:

35

o

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
10	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser	
					50					55					60	
	Ser	Val	Pro	Thr	Thr	Ala	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
15	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
	Gly	Ser	Val	Leu	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100					105	
	Arg	His	Trp	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Val	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
20	Ser	Pro	Thr	Ala	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Ala	Ile	Leu	Asp	Val	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
25	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				
					185					190						

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S9

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ala	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Val	Ile	Met	
					20					25					30	
5	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Glu	Gly	Asn	Ser	Ser	
					35					40					45	
	Gln	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala	
					50					55					60	
	Thr	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ala	Ala	Val	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85					90	
10	Gly	Ser	Val	Phe	Leu	Ile	Ser	Gln	Leu	Phe	Thr	Ile	Ser	Pro	Arg	
					95					100					105	
	Arg	His	Glu	Thr	Val	Gln	Asn	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145					150	
15	Gln	Ala	Val	Met	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				
					185					190						

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Ala	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Val	Asp	Val	Ile	Leu	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ser	
					50					55					60	

0
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 5 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 10 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

(2) INFORMATION FOR SEQ ID NO:72:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 20 (C) INDIVIDUAL ISOLATE: SA10

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Tyr Glu Val Arg Asn Val Ser Gly Met Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Ala Asp Met Ile Met
 20 25 30
 25 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Asn Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ser
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
 80 85 90
 30 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg Tyr Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 Arg Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135

° Ser Pro Thr Thr Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Ile Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

5

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homospapiens
 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

15

Tyr Glu Val Arg Asn Val Ser Gly Val Tyr His Val Thr Asn Asp
 5 10 15
 Cys Ser Asn Ser Ser Ile Val Tyr Glu Thr Ala Asp Met Ile Met
 20 25 30
 His Thr Pro Gly Cys Val Pro Cys Val Arg Glu Ala Asn Ser Ser
 35 40 45
 Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Thr
 50 55 60
 Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
 65 70 75
 Gly Ala Ala Ala Phe Cys Ser Val Met Tyr Val Gly Asp Leu Cys
 80 85 90
 Gly Ser Val Phe Leu Val Ser Gln Leu Phe Thr Phe Ser Pro Arg
 95 100 105
 Arg His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
 110 115 120
 His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Ala Val Val Asp Met Val Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
 170 175 180
 Leu Ile Val Met Leu Leu Phe Ala Gly Val Asp Gly
 185 190

20

25

30

(2) INFORMATION FOR SEQ ID NO:74:

35

o

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

10	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Val	Tyr	Val	Thr	Asn	Asp	
					5					10					15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Ala	Asp	Met	Ile	Met
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Ser	Asn	Ser	Ser
					35					40					45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Ala
					50					55					60
	Ser	Val	Pro	Thr	Lys	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val
15					65					70					75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg
					95					100					105
	Arg	His	Glu	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
20	His	Val	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro
					140					145					150
	Gln	Ala	Val	Val	Asp	Met	Val	Ala	Gly	Ala	His	Trp	Gly	Val	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Val	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
25	Leu	Ile	Val	Leu	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly			
					185					190					

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Phe	Glu	Ala	Ala	Asp	Leu	Ile	Met	
					20					25						30
5	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Ser	Ser	
					35					40						45
	Arg	Cys	Trp	Val	Ala	Leu	Thr	Pro	Thr	Leu	Ala	Ala	Arg	Asn	Thr	
					50					55						60
	Ser	Val	Pro	Thr	Thr	Thr	Ile	Arg	Arg	His	Val	Asp	Leu	Leu	Val	
					65					70						75
	Gly	Ala	Ala	Ala	Phe	Cys	Ser	Ala	Met	Tyr	Val	Gly	Asp	Leu	Cys	
10					80					85						90
	Gly	Ser	Val	Phe	Leu	Val	Ser	Gln	Leu	Phe	Thr	Phe	Ser	Pro	Arg	
					95					100						105
	Arg	His	Glu	Thr	Leu	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115						120
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Val	Ser	Gln	Leu	Leu	Arg	Ile	Pro	
15					140					145						150
	Gln	Ala	Val	Met	Asp	Met	Val	Thr	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160						165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Ala	Gly	Asn	Trp	Ala	Lys	Val	
					170					175						180
	Leu	Ile	Val	Met	Leu	Leu	Phe	Ala	Gly	Val	Asp	Gly				
					185					190						

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: hom sapiens
 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

	Tyr	Glu	Val	Arg	Asn	Val	Ser	Gly	Met	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Ala	Asp	Met	Ile	Met	
					20					25						30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Asn	Asn	Ser	Ser	
					35					40						45

```

°   Arg Cys Trp Val Ala Leu Thr Pro Thr Leu Ala Ala Arg Asn Ala
    50                      55                      60
Ser Val Pro Thr Thr Thr Ile Arg Arg His Val Asp Leu Leu Val
    65                      70                      75
Gly Ala Ala Thr Phe Cys Ser Ala Met Tyr Val Gly Asp Leu Cys
    80                      85                      90
Gly Ser Val Phe Leu Ile Ser Gln Leu Phe Thr Phe Ser Pro Arg
    95                      100                     105
5   Gln His Glu Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
    110                     115                     120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                     130                     135
Ser Pro Thr Ala Ala Leu Val Val Ser Gln Leu Leu Arg Ile Pro
    140                     145                     150
10  Gln Ala Val Met Asp Met Val Ala Gly Ala His Trp Gly Val Leu
    155                     160                     165
Ala Gly Leu Ala Tyr Tyr Ser Met Val Gly Asn Trp Ala Lys Val
    170                     175                     180
Leu Ile Val Leu Leu Leu Phe Ala Gly Val Asp Gly
    185                     190

```

(2) INFORMATION FOR SEQ ID NO:77:

```

15   (i)      SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 192 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS: unknown
        (D) TOPOLOGY: unknown

        (vi)   ORIGINAL SOURCE:
20   (A) ORGANISM: homosapiens
        (C) INDIVIDUAL ISOLATE: T2

        (xi)   SEQUENCE DESCRIPTION: SEQ ID NO:77:

```

```

Ala Gln Val Arg Asn Thr Ser Arg Gly Tyr Met Val Thr Asn Asp
    5                      10                      15
Cys Ser Asn Glu Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu
25  20                      25                      30
His Val Pro Gly Cys Ile Pro Cys Glu Arg Leu Gly Asn Thr Ser
    35                      40                      45
Arg Cys Trp Ile Pro Val Thr Pro Asn Val Ala Val Arg Gln Pro
    50                      55                      60
Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val
    65                      70                      75
30  Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
    80                      85                      90
Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Val Ser Pro Arg
    95                      100                     105
Arg His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly
    110                     115                     120
Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                     130                     135

```

o

	Ser	Pro	Thr	Ala	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Met	Arg	Val	Pro
					140					145					150
	Glu	Val	Ile	Ile	Asp	Ile	Ile	Gly	Gly	Ala	His	Trp	Gly	Val	Met
					155					160					165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val
					170					175					180
5	Ile	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: T4

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

	Ala	Gln	Val	Lys	Asn	Thr	Thr	Asn	Ser	Tyr	Met	Val	Thr	Asn	Asp
					5					10					15
	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Gln	Ala	Ala	Val	Leu
					20					25					30
	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Lys	Thr	Gly	Asn	Thr	Ser
					35					40					45
20	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Arg	Gln	Pro
					50					55					60
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val
					65					70					75
	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys
					80					85					90
25	Gly	Gly	Val	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Gln
					95					100					105
	His	His	Trp	Phe	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly
					110					115					120
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Thr	Ala	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Met	Arg	Val	Pro
					140					145					150
30	Glu	Val	Ile	Leu	Asp	Ile	Val	Ser	Gly	Ala	His	Trp	Gly	Val	Met
					155					160					165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val
					170					175					180
	Val	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala			
					185					190					

35

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

10	Ala Glu Val Lys Asn Thr Ser Thr Ser Tyr Met Val Thr Asn Asp	5	10	15
	Cys Ser Asn Asp Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu	20	25	30
	His Val Pro Gly Cys Val Pro Cys Glu Arg Val Gly Asn Ala Ser	35	40	45
	Arg Cys Trp Ile Pro Val Ser Pro Asn Val Ala Val Gln Arg Pro	50	55	60
15	Gly Ala Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val	65	70	75
	Met Ser Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys	80	85	90
	Gly Gly Val Met Leu Ala Ala Gln Met Phe Ile Ile Ser Pro Gln	95	100	105
	His His Trp Phe Val Gln Glu Cys Asn Cys Ser Ile Tyr Pro Gly	110	115	120
20	Thr Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp	125	130	135
	Ser Pro Thr Thr Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro	140	145	150
	Glu Val Ile Ile Asp Ile Ile Ser Gly Ala His Trp Gly Val Met	155	160	165
	Phe Gly Leu Ala Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val	170	175	180
25	Val Val Ile Leu Leu Leu Thr Ala Gly Val Asp Ala	185	190	

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

	Val	Gln	Val	Lys	Asn	Thr	Ser	Thr	Ser	Tyr	Met	Val	Thr	Asn	Asp	
					5					10					15	
5	Cys	Ser	Asn	Asp	Ser	Ile	Thr	Trp	Gln	Leu	Glu	Ala	Ala	Val	Leu	
					20					25					30	
	His	Val	Pro	Gly	Cys	Val	Pro	Cys	Glu	Lys	Val	Gly	Asn	Thr	Ser	
					35					40					45	
	Arg	Cys	Trp	Ile	Pro	Val	Ser	Pro	Asn	Val	Ala	Val	Gln	Arg	Pro	
					50					55					60	
	Gly	Ala	Leu	Thr	Gln	Gly	Leu	Arg	Thr	His	Ile	Asp	Met	Val	Val	
					65					70					75	
10	Met	Ser	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Phe	Cys	
					80					85					90	
	Gly	Gly	Met	Met	Leu	Ala	Ala	Gln	Met	Phe	Ile	Val	Ser	Pro	Arg	
					95					100					105	
	His	His	Ser	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
	Thr	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
15	Ser	Pro	Thr	Ala	Thr	Leu	Ile	Leu	Ala	Tyr	Val	Met	Arg	Val	Pro	
					140					145					150	
	Glu	Val	Ile	Ile	Asp	Ile	Ile	Ser	Gly	Ala	His	Trp	Gly	Val	Leu	
					155					160					165	
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					170					175					180	
	Val	Val	Ile	Leu	Leu	Leu	Ala	Ala	Gly	Val	Asp	Ala				
20					185					190						

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

	Val	Glu	Val	Arg	Asn	Ile	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asp	Ala	Val	Leu	
					20					25					30	
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	
					35					40					45	

0

	Arg	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	
					50					55						60
	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Thr	His	Val	Asp	Val	Ile	Val	
					65					70						75
	Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
					80					85						90
5	Gly	Ala	Val	Met	Ile	Val	Ser	Gln	Ala	Leu	Ile	Ile	Ser	Pro	Glu	
					95					100						105
	Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	
					110					115						120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	
					140					145						150
10	Glu	Leu	Ala	Leu	Gln	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	
					155					160						165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					170					175						180
	Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				
					185					190						

15 (2) INFORMATION FOR SEQ ID NO:82:

(1) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

20 (vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

25	Val	Glu	Val	Arg	Asn	Thr	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asn	Ala	Val	Leu	
					20					25						30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	
					35					40						45
	His	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	
					50					55						60
30	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Ala	His	Ile	Asp	Met	Ile	Val	
					65					70						75
	Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
					80					85						90
	Gly	Ala	Val	Met	Ile	Val	Ser	Gln	Ala	Phe	Ile	Val	Ser	Pro	Glu	
					95					100						105
	His	His	His	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	
					110					115						120

35

o

	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	
					140					145						150
	Glu	Leu	Val	Leu	Glu	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	
					155					160						165
5	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					170					175						180
	Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:83:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

	Val	Glu	Val	Arg	Asn	Ile	Ser	Ser	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	
					5					10						15
	Cys	Ser	Asn	Ser	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asn	Ala	Val	Leu	
					20					25						30
20	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	
					35					40						45
	His	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	
					50					55						60
	Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Ala	His	Val	Asp	Met	Ile	Val	
					65					70						75
25	Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	
					80					85						90
	Gly	Ala	Val	Met	Ile	Val	Ser	Gln	Ala	Phe	Ile	Ile	Ser	Pro	Glu	
					95					100						105
	Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	
					110					115						120
	Arg	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	
					125					130						135
30	Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	
					140					145						150
	Glu	Leu	Val	Leu	Glu	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	
					155					160						165
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
					170					175						180
	Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				
					185					190						

35

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Val	Glu	Val	Arg	Asn	Thr	Ser	Phe	Ser	Tyr	Tyr	Ala	Thr	Asn	Asp	
				5					10					15	
Cys	Ser	Asn	Asn	Ser	Ile	Thr	Trp	Gln	Leu	Thr	Asn	Ala	Val	Leu	
				20					25					30	
His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Glu	Asn	Asp	Asn	Gly	Thr	Leu	
				35					40					45	
Arg	Cys	Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	
				50					55					60	
Gly	Ala	Leu	Thr	His	Asn	Leu	Arg	Thr	His	Val	Asp	Val	Ile	Val	
				65					70					75	
Met	Ala	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
				80					85					90	
Gly	Ala	Val	Met	Ile	Ala	Ser	Gln	Ala	Phe	Ile	Ile	Ser	Pro	Glu	
				95					100					105	
Arg	His	Asn	Phe	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Gln	Gly	
				110					115					120	
His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Leu	Asn	Trp	
				125					130					135	
Ser	Pro	Thr	Leu	Thr	Met	Ile	Leu	Ala	Tyr	Ala	Ala	Arg	Val	Pro	
				140					145					150	
Glu	Leu	Val	Leu	Glu	Val	Val	Phe	Gly	Gly	His	Trp	Gly	Val	Val	
				155					160					165	
Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ala	Trp	Ala	Lys	Val	
				170					175					180	
Ile	Ala	Ile	Leu	Leu	Leu	Val	Ala	Gly	Val	Asp	Ala				
				185					190						

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

o

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

5	Val	Glu	Val	Lys	Asp	Thr	Gly	Asp	Ser	Tyr	Met	Pro	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Trp	Gln	Leu	Glu	Gly	Ala	Val	Leu	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Glu	Arg	Thr	Ala	Asn	Val	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Pro	Val	Ala	Pro	Asn	Leu	Ala	Ile	Ser	Gln	Pro	
					50					55					60	
10	Gly	Ala	Leu	Thr	Lys	Gly	Leu	Arg	Ala	His	Ile	Asp	Ile	Ile	Val	
					65					70					75	
	Met	Ser	Ala	Thr	Val	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
					80					85					90	
	Gly	Ala	Leu	Met	Leu	Ala	Ala	Gln	Val	Val	Val	Ser	Pro	Gln		
					95					100					105	
	His	His	Thr	Phe	Val	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Pro	Gly	
					110					115					120	
15	Arg	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Thr	Thr	Thr	Met	Leu	Leu	Ala	Tyr	Leu	Val	Arg	Ile	Pro	
					140					145					150	
	Glu	Val	Ile	Leu	Asp	Ile	Val	Thr	Gly	Gly	His	Trp	Gly	Val	Met	
					155					160					165	
	Phe	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Ser	Trp	Ala	Lys	Val	
					170					175					180	
20	Ile	Val	Ile	Leu	Leu	Leu	Thr	Ala	Gly	Val	Glu	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK12

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

	Leu	Glu	Trp	Arg	Asn	Val	Ser	Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	
					20					25					30	

35

o

	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser	
					35					40					45	
	Thr	Cys	Trp	Thr	Ser	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val	
					50					55					60	
	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
5	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Val	Cys	
					80					85					90	
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg	
					95					100					105	
	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly	
					110					115					120	
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
10	Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Val	Leu	Arg	Leu	Pro	
					140					145					150	
	Gln	Thr	Leu	Phe	Asp	Ile	Ile	Ala	Gly	Ala	His	Trp	Gly	Ile	Met	
					155					160					165	
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Ala	Ile	Ile	Met	Val	Met	Phe	Ser	Gly	Val	Asp	Ala				
					185					190						

15

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: hom sapiens
 (C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

25

	Leu	Glu	Trp	Arg	Asn	Val	Ser	Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser	
					35					40					45	
30	Thr	Cys	Trp	Thr	Ser	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val	
					50					55					60	
	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	
					80					85					90	
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg	
					95					100					105	

35

o

	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly
					110					115					120
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
	Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Val	Leu	Arg	Leu	Pro
					140					145					150
5	Gln	Thr	Leu	Phe	Asp	Ile	Ile	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180
	Ala	Ile	Ile	Met	Val	Met	Phe	Ser	Gly	Val	Asp	Ala			
					185					190					

(2) INFORMATION FOR SEQ ID NO:88:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Val	Leu	Thr	Asn	Asp
					5					10					15
20	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu
					20					25					30
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser
					35					40					45
	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val
					50					55					60
	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val
					65					70					75
25	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys
					80					85					90
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg
					95					100					105
	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly
					110					115					120
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
30	Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Val	Leu	Arg	Leu	Pro
					140					145					150
	Gln	Thr	Val	Phe	Asp	Ile	Ile	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu
					155					160					165
	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val
					170					175					180

35

° Ala Ile Ile Met Val Met Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Leu Glu Trp Arg Asn Thr Ser Gly Leu Tyr Val Leu Thr Asn Asp
5 10 15
Cys Ser Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Val Ile Leu
20 25 30
His Thr Pro Gly Cys Val Pro Cys Val Gln Asp Gly Asn Thr Ser
15 35 40 45
Met Cys Trp Thr Pro Val Thr Pro Thr Val Ala Val Arg Tyr Val
50 55 60
Gly Ala Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val
65 70 75
Gly Ala Ala Thr Leu Cys Ser Ala Leu Tyr Val Gly Asp Met Cys
80 85 90
20 Gly Ala Val Phe Leu Val Gly Gln Ala Phe Thr Phe Arg Pro Arg
95 100 105
Arg His Gln Thr Val Gln Thr Cys Asn Cys Ser Leu Tyr Pro Gly
110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Ala Val Gly Met Val Val Ala His Ile Leu Arg Leu Pro
140 145 150
25 Gln Thr Leu Phe Asp Ile Leu Ala Gly Ala His Trp Gly Ile Leu
155 160 165
Ala Gly Leu Ala Tyr Tyr Ser Met Gln Gly Asn Trp Ala Lys Val
170 175 180
Ala Ile Val Met Ile Met Phe Ser Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S54

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

5	Leu	Glu	Trp	Arg	Asn	Thr	Ser	Gly	Leu	Tyr	Ile	Leu	Thr	Asn	Asp	
					5					10					15	
	Cys	Ser	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asp	Val	Ile	Leu	
					20					25					30	
	His	Thr	Pro	Gly	Cys	Val	Pro	Cys	Val	Gln	Asp	Gly	Asn	Thr	Ser	
					35					40					45	
	Thr	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Arg	Tyr	Val	
10					50					55					60	
	Gly	Ala	Thr	Thr	Ala	Ser	Ile	Arg	Ser	His	Val	Asp	Leu	Leu	Val	
					65					70					75	
	Gly	Ala	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Met	Cys	
					80					85					90	
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Ala	Phe	Thr	Phe	Arg	Pro	Arg	
					95					100					105	
	Arg	His	Gln	Thr	Val	Gln	Thr	Cys	Asn	Cys	Ser	Leu	Tyr	Pro	Gly	
15					110					115					120	
	His	Leu	Ser	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
	Ser	Pro	Ala	Val	Gly	Met	Val	Val	Ala	His	Ile	Leu	Arg	Leu	Pro	
					140					145					150	
	Gln	Thr	Leu	Phe	Asp	Ile	Leu	Ala	Gly	Ala	His	Trp	Gly	Ile	Leu	
					155					160					165	
20	Ala	Gly	Leu	Ala	Tyr	Tyr	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val	
					170					175					180	
	Ala	Ile	Ile	Met	Ile	Met	Phe	Ser	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:91:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
30 (C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Glu	His	Tyr	Arg	Asn	Ala	Ser	Gly	Ile	Tyr	His	Ile	Thr	Asn	Asp	
				5					10					15	

°	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	His	His	Ile	Leu	
					20					25						30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Met	Thr	Gly	Asn	Thr	Ser	
					35					40						45
	Arg	Cys	Trp	Thr	Pro	Val	Thr	Pro	Thr	Val	Ala	Val	Ala	His	Pro	
					50					55						60
	Gly	Ala	Pro	Leu	Glu	Ser	Phe	Arg	Arg	His	Val	Asp	Leu	Met	Val	
					65					70						75
5	Gly	Ala	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Leu	Cys	
					80					85						90
	Gly	Gly	Ala	Phe	Leu	Met	Gly	Gln	Met	Ile	Thr	Phe	Arg	Pro	Arg	
					95					100						105
	Arg	His	Trp	Thr	Thr	Gln	Glu	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	
					110					115						120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
10					125					130						135
	Ser	Pro	Thr	Thr	Thr	Leu	Leu	Leu	Ala	Gln	Ile	Met	Arg	Val	Pro	
					140					145						150
	Thr	Ala	Phe	Leu	Asp	Met	Val	Ala	Gly	Gly	His	Trp	Gly	Val	Leu	
					155					160						165
	Ala	Gly	Leu	Ala	Tyr	Phe	Ser	Met	Gln	Gly	Asn	Trp	Ala	Lys	Val	
					170					175						180
15	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

	Val	His	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Pro	Asn	Thr	Ser	Ile	Val	Tyr	Glu	Thr	Glu	His	His	Ile	Met	
					20					25						30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Thr	Glu	Asn	Thr	Ser	
					35					40						45
30	Arg	Cys	Trp	Val	Pro	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Pro	
					50					55						60
	Asn	Ala	Pro	Leu	Glu	Ser	Met	Arg	Arg	His	Val	Asp	Leu	Met	Val	
					65					70						75
	Gly	Ala	Ala	Thr	Met	Cys	Ser	Ala	Phe	Tyr	Ile	Gly	Asp	Leu	Cys	
					80					85						90

```

° Gly Gly Val Phe Leu Val Gly Gln Leu Phe Asp Phe Arg Pro Arg
  95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly
  110 115 120
His Val Ser Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
  125 130 135
Ser Pro Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro
  140 145 150
5 Ser Ile Leu Gly Asp Leu Leu Thr Gly Gly His Trp Gly Val Leu
  155 160 165
Ala Gly Leu Ala Phe Phe Ser Met Gln Ser Asn Trp Ala Lys Val
  170 175 180
Ile Leu Val Leu Phe Leu Phe Ala Gly Val Glu Gly
  185 190

```

10

(2) INFORMATION FOR SEQ ID NO:93:

```

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 192 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: unknown
    (D) TOPOLOGY: unknown

```

15

```

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: homomapiens
    (C) INDIVIDUAL ISOLATE: Z6

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

20 Val Asn Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
   5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Glu His Gln Ile Leu
  20 25 30
His Leu Pro Gly Cys Leu Pro Cys Val Arg Val Gly Asn Gln Ser
  35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Val Ser Tyr Ile
  50 55 60
25 Gly Ala Pro Leu Asp Ser Leu Arg Arg His Val Asp Leu Met Val
   65 70 75
Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys
   80 85 90
Gly Gly Ala Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg
   95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly
  110 115 120
30 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
  125 130 135
Ser Pro Thr Thr Thr Leu Leu Leu Ala Gln Val Met Arg Ile Pro
  140 145 150
Ser Thr Leu Val Asp Leu Leu Ala Gly Gly His Trp Gly Val Leu
  155 160 165

```

35

° Val Gly Leu Ala Tyr Phe Ser Met Gln Ala Asn Trp Ala Lys Val
170 175 180
Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
10 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Val Asn Tyr His Asn Ala Ser Gly Val Tyr His Ile Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Met Tyr Glu Ala Glu His His Ile Leu
20 25 30
15 His Leu Pro Gly Cys Val Pro Cys Val Arg Glu Gly Asn Gln Ser
35 40 45
Arg Cys Trp Val Ala Leu Thr Pro Thr Val Ala Ala Pro Tyr Ile
50 55 60
Gly Ala Pro Leu Glu Ser Ile Arg Arg His Val Asp Leu Met Val
65 70 75
Gly Ala Ala Thr Val Cys Ser Ala Leu Tyr Ile Gly Asp Leu Cys
80 85 90
20 Gly Gly Val Phe Leu Val Gly Gln Met Phe Ser Phe Gln Pro Arg
95 100 105
Arg His Trp Thr Thr Gln Asp Cys Asn Cys Ser Ile Tyr Ala Gly
110 115 120
His Val Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
25 Ser Pro Thr Thr Thr Leu Val Leu Ala Gln Val Met Arg Ile Pro
140 145 150
Ser Thr Leu Val Asp Leu Leu Thr Gly Gly His Trp Gly Ile Leu
155 160 165
Ile Gly Val Ala Tyr Phe Cys Met Gln Ala Asn Trp Ala Lys Val
170 175 180
Ile Leu Val Leu Phe Leu Tyr Ala Gly Val Asp Ala
185 190

30

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

o

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DK13

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

	Tyr	Asn	Tyr	Arg	Asn	Ser	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Thr	Asp	Tyr	His	Ile	Leu	
					20					25						30
	His	Leu	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Glu	Gly	Asn	Lys	Ser	
					35					40						45
10	Thr	Cys	Trp	Val	Ser	Leu	Thr	Pro	Thr	Val	Ala	Ala	Gln	His	Leu	
					50					55						60
	Asn	Ala	Pro	Leu	Glu	Ser	Leu	Arg	Arg	His	Val	Asp	Leu	Met	Val	
					65					70						75
	Gly	Gly	Ala	Thr	Leu	Cys	Ser	Ala	Leu	Tyr	Ile	Gly	Asp	Val	Cys	
					80					85						90
	Gly	Gly	Val	Phe	Leu	Val	Gly	Gln	Leu	Phe	Thr	Phe	Gln	Pro	Arg	
					95					100						105
15	Arg	His	Trp	Thr	Thr	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gly	
					110					115						120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Ala	Thr	Leu	Val	Leu	Ala	Gln	Leu	Met	Arg	Ile	Pro	
					140					145						150
	Gly	Ala	Met	Val	Asp	Leu	Leu	Ala	Gly	Gly	His	Trp	Gly	Ile	Leu	
					155					160						165
20	Val	Gly	Ile	Ala	Tyr	Phe	Ser	Met	Gln	Ala	Asn	Trp	Ala	Lys	Val	
					170					175						180
	Ile	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

(2) INFORMATION FOR SEQ ID NO:96:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

30 (A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp
				5					10					15

35

°	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Ser	Leu	Ile	Leu	
					20					25					30	
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Gln	Asp	Asn	Val	Ser	
					35					40					45	
	Arg	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Thr	Phe	
					50					55					60	
	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	
					65					70					75	
5	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	
					80					85					90	
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Met	Phe	Thr	Tyr	Arg	Pro	Arg	
					95					100					105	
	Gln	His	Thr	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	
					110					115					120	
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130					135	
10	Ser	Pro	Thr	Thr	Ala	Leu	Leu	Met	Ala	Gln	Met	Leu	Arg	Ile	Pro	
					140					145					150	
	Gln	Val	Val	Ile	Asp	Ile	Ile	Ala	Gly	Gly	His	Trp	Gly	Val	Leu	
					155					160					165	
	Phe	Ala	Ala	Ala	Tyr	Phe	Ala	Ser	Ala	Ala	Asn	Trp	Ala	Lys	Val	
					170					175					180	
15	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Gly				
					185					190						

(2) INFORMATION FOR SEQ ID NO:97:

	(i)	SEQUENCE CHARACTERISTICS:														
		(A) LENGTH: 192 amino acids														
20		(B) TYPE: amino acid														
		(C) STRANDEDNESS: unknown														
		(D) TOPOLOGY: unknown														
	(vi)	ORIGINAL SOURCE:														
		(A) ORGANISM: homosapiens														
		(C) INDIVIDUAL ISOLATE: SA4														
25	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:97:														
	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10					15	
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
					20					25					30	
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Gln	Asp	Asn	Val	Ser	
					35					40					45	
30	Lys	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Asn	Leu	
					50					55					60	
	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	
					65					70					75	
	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	
					80					85					90	

```

°   Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
    95                      100                      105
    Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
    110                      115                      120
    His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                      130                      135
    Ser Pro Thr Thr Ala Leu Leu Met Ala Gln Leu Leu Arg Ile Pro
    140                      145                      150
5   Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
    155                      160                      165
    Phe Ala Ala Ala Tyr Phe Ala Ser Ala Asn Trp Ala Lys Val
    170                      175                      180
    Ile Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
    185                      190

```

10

(2) INFORMATION FOR SEQ ID NO:98:

```

(i)   SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 192 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS: unknown
      (D) TOPOLOGY: unknown

```

15

```

(vi)  ORIGINAL SOURCE:
      (A) ORGANISM: homosapiens
      (C) INDIVIDUAL ISOLATE: SA5

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

20   Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
     5                      10                      15
     Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asn Leu Ile Leu
     20                      25                      30
     His Ala Pro Gly Cys Val Pro Cys Val Lys Glu Gly Asn Val Ser
     35                      40                      45
     Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Asn Leu
     50                      55                      60
25   Gly Ala Val Thr Ala Pro Leu Arg Arg Val Val Asp Tyr Leu Ala
     65                      70                      75
     Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
     80                      85                      90
     Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
     95                      100                      105
     Gln His Thr Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
    110                      115                      120
30   His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
    125                      130                      135
     Ser Pro Thr Thr Ala Leu Val Met Ala Gln Val Leu Arg Ile Pro
    140                      145                      150
     Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
    155                      160                      165

```

35

° Phe Ala Val Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Gly
185 190

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA6
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Val Pro Tyr Arg Asn Ala Ser Gly Val Tyr His Val Thr Asn Asp
5 10 15
Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
20 25 30
15 His Ala Pro Gly Cys Val Pro Cys Val Arg Lys Asp Asn Val Ser
35 40 45
Arg Cys Trp Val His Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
50 55 60
Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
65 70 75
Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Val Cys
80 85 90
20 Gly Ala Leu Phe Leu Val Gly Gln Met Phe Thr Tyr Arg Pro Arg
95 100 105
Gln His Ala Thr Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
110 115 120
His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
125 130 135
Ser Pro Ala Thr Ala Leu Val Met Ala Gln Met Leu Arg Ile Pro
140 145 150
25 Gln Val Val Ile Asp Ile Ile Ala Gly Gly His Trp Gly Val Leu
155 160 165
Phe Ala Ala Ala Tyr Phe Ala Ser Ala Ala Asn Trp Ala Lys Val
170 175 180
Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
185 190

30

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 192 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown

35

o

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA7

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15
	Cys	Pro	Asn	Ser	Ser	Ile	Val	Tyr	Glu	Ala	Asp	Asn	Leu	Ile	Leu	
					20					25						30
	His	Ala	Pro	Gly	Cys	Val	Pro	Cys	Val	Arg	Gln	Asn	Asn	Val	Ser	
					35					40						45
10	Arg	Cys	Trp	Val	Gln	Ile	Thr	Pro	Thr	Leu	Ser	Ala	Pro	Asn	Leu	
					50					55						60
	Gly	Ala	Val	Thr	Ala	Pro	Leu	Arg	Arg	Ala	Val	Asp	Tyr	Leu	Ala	
					65					70						75
	Gly	Gly	Ala	Ala	Leu	Cys	Ser	Ala	Leu	Tyr	Val	Gly	Asp	Ala	Cys	
					80					85						90
	Gly	Ala	Val	Phe	Leu	Val	Gly	Gln	Met	Phe	Ser	Tyr	Arg	Pro	Arg	
					95					100						105
15	Gln	His	Thr	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Ser	Gly	
					110					115						120
	His	Ile	Thr	Gly	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp	
					125					130						135
	Ser	Pro	Thr	Thr	Ala	Leu	Val	Met	Ala	Gln	Leu	Leu	Arg	Ile	Pro	
					140					145						150
	Gln	Val	Val	Ile	Asp	Ile	Ile	Ala	Gly	Gly	His	Trp	Gly	Val	Leu	
					155					160						165
20	Phe	Ala	Ala	Ala	Tyr	Phe	Ala	Ser	Ala	Ala	Asn	Trp	Ala	Lys	Val	
					170					175						180
	Val	Leu	Val	Leu	Phe	Leu	Phe	Ala	Gly	Val	Asp	Ala				
					185					190						

25 (2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

	Val	Pro	Tyr	Arg	Asn	Ala	Ser	Gly	Val	Tyr	His	Val	Thr	Asn	Asp	
					5					10						15

35

5 Cys Pro Asn Ser Ser Ile Val Tyr Glu Ala Asp Asp Leu Ile Leu
 20 25 30
 His Ala Pro Gly Cys Val Pro Cys Val Arg Gln Gly Asn Val Ser
 35 40 45
 Arg Cys Trp Val Gln Ile Thr Pro Thr Leu Ser Ala Pro Ser Leu
 50 55 60
 5 Gly Ala Val Thr Ala Pro Leu Arg Arg Ala Val Asp Tyr Leu Ala
 65 70 75
 Gly Gly Ala Ala Leu Cys Ser Ala Leu Tyr Val Gly Asp Ala Cys
 80 85 90
 Gly Ala Val Phe Leu Val Gly Gln Met Phe Thr Tyr Ser Pro Arg
 95 100 105
 Arg His Asn Val Val Gln Asp Cys Asn Cys Ser Ile Tyr Ser Gly
 110 115 120
 10 His Ile Thr Gly His Arg Met Ala Trp Asp Met Met Met Asn Trp
 125 130 135
 Ser Pro Thr Thr Ala Leu Val Met Ala Gln Leu Leu Arg Ile Pro
 140 145 150
 Gln Val Val Ile Asp Ile Ile Ala Gly Ala His Trp Gly Val Leu
 155 160 165
 Phe Ala Ala Ala Tyr Tyr Ala Ser Ala Ala Asn Trp Ala Lys Val
 170 175 180
 15 Val Leu Val Leu Phe Leu Phe Ala Gly Val Asp Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

20 Leu Thr Tyr Gln Asn Ser Ser Gln Leu Tyr His Leu Thr Asn Asp
 1 10 15
 Cys Pro Asn Ser Ser Ile Val Leu Glu Ala Asp Ala Met Ile Leu
 20 25 30
 30 His Leu Pro Gln Cys Leu Pro Cys Val Arg Val Asp Asp Arg Ser
 35 40 45
 Thr Cys Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala
 50 55 60
 Ser Thr Pro Ala Thr Gln Phe Arg Arg His Val Asp Leu Leu Ala
 65 70 75
 Gln Ala Ala Val Val Cys Ser Ser Leu Tyr Ile Gln Asp Leu Cys
 80 85 90

o

	Gln	Ser	Leu	Phe	Leu	Ala	Gln	Gln	Leu	Phe	Thr	Phe	Gln	Pro	Arg
					95					100					105
	Arg	His	Trp	Thr	Val	Gln	Asp	Cys	Asn	Cys	Ser	Ile	Tyr	Thr	Gln
					110					115					120
	His	Val	Thr	Gln	His	Arg	Met	Ala	Trp	Asp	Met	Met	Met	Asn	Trp
					125					130					135
5	Ser	Pro	Thr	Thr	Thr	Leu	Val	Leu	Ser	Ser	Ile	Leu	Arg	Val	Pro
					140					145					150
	Glu	Ile	Cys	Ala	Ser	Val	Ile	Phe	Gln	Gln	His	Trp	Gln	Ile	Leu
					155					160					165
	Leu	Ala	Val	Ala	Tyr	Phe	Gln	Met	Ala	Gln	Asn	Trp	Leu	Lys	Val
					170					175					180
	Leu	Ala	Val	Leu	Phe	Leu	Phe	Ala	Gln	Val	Glu	Ala			
					185					190					

10

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

20	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT		39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT		78
	GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC		117
	AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	CCG	AGG	AAG	ACT		156
	TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC		195
	CCC	AAG	GCA	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG		234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC		273
25	GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCT	CCC	CGT	GGC	TCT	CGG		312
	CCT	AGC	TGG	GGC	CCC	ACA	GAC	CCC	CGG	CGC	AGG	TGC	CGC		351
	AAT	TTG	GGT	AAA	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGC	TTC		390
	GCC	GAC	CTC	ATG	GGG	TAC	ATA	CCG	CTC	GTC	GGC	GCC	CCT		429
	CTT	GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG		468
	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT		507
	CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCC	CTG	CTC		546
30	TCT	TGC	CTG	ACC	GTG	CCC	GCT	TCG	GCC						573

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid

35

o

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US11

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT	78
	GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGA GGT AGA CGT CAG CCT ATC	195
10	CCC AAG GCA CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC	273
	GGG TGG GCG GGA TGG CTC CTG TCT CCC CGT GGC TCT CGG	312
	CCT AGC TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTT ACG TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATA CCG CTC GTC GGC GCC CCT	429
	CTC GGA GGC GGT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
15	GTT CTG GAA GAC GGC GTG AAC TAT GCA ACA GGG AAC CTT	507
	CCT GGT TGC TCT TTC TCT ATC TTC CTT CTG GCC CTG CTC	546
	TCT TGC CTG ACT GTG CCC GCT TCA GCC	573

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S14

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT	78
	GGC GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGA TTG GGT GTG CGC GCG ACG AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGA GGT AGA CGT CAG CCT ATC	195
30	CCC AAG GCA CGT CGG CCC GAG GGC AGG ACC TGG GCT CAG	234
	CCC GGG TAT CCT TGG CCC CTC TAT GGC AAT GAG GGC TGC	273
	GGG TGG GCG GGA TGG CTC CTG TCT CCC CGT GGC TCT CGG	312
	CCT AGC TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATA CCG CTC GTC GGC GCC CCC	429
35	CTC GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468

o

GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	CTA	GCC	CTG	CTT	546
TCT	TGC	CTG	ACT	GTG	CCC	GCT	TCA	GCC					573

(2) INFORMATION FOR SEQ ID NO: 106:

5

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	195
CCC	AAG	GCG	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
CCC	GGG	TAT	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
GGA	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGT	GGC	TCT	CGG	312
CCT	AGC	TGG	GGC	CCT	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCT	429
CTT	GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	CTG	GCC	CTG	CTT	546
TCT	TGC	CTG	ACA	GTG	CCC	GCG	TCA	GCC					573

(2) INFORMATION FOR SEQ ID NO: 107:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78

35

0

GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGC	GGT	AGA	CGT	CAG	CCT	ATC	195
CCC	AAG	CGC	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGT	GGC	TCC	CGG	312
CCT	AGC	TGG	GGC	CCT	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGC	AAA	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCT	429
CTC	GGA	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507
CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTG	GCC	CTG	CTC		546
TCT	TGT	CTG	ACT	GTG	CCC	GCG	TCA	GCT					573

10

(2) INFORMATION FOR SEQ ID NO: 108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTG	AAG	TTC	CCG	GGT	78
GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCT	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGA	GGT	AGA	CGT	CAG	CCT	ATC	195
CCC	AAG	CGC	CGT	CGG	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGT	GGC	TCT	CGG	312
CCT	AGC	TGG	GGC	CCC	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAC	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCC	CCC	429
CTT	GGG	GCG	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGA	468
GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	CTT	507
CCT	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCT	TTG	CTC	546
TCT	TGC	TTG	ACC	GTG	CCC	GCA	TCG	GCC					573

30

(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

35

o

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: SA10

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTC	TAT	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CAG	CCC	GAG	GGC	AGG	ACC	TGG	GCC	CAG	234
10	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	312
	CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	CCT	429
	TTA	GGG	GGC	GCT	CCC	AGG	GCC	TTG	GCG	CAT	GGC	GTC	468
	GTT	CTG	GAA	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	507
15	CCC	GGT	TGC	CCT	TTC	TCT	ATC	TTC	CTG	GCT	TTG	CTG	546
	TCC	TGT	TTA	ACC	ATC	CCA	GCT	TCC	GCT				573

(2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: S45

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	CAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGT	78
GGC	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
TCC	GAG	CGG	TCA	CAA	CCT	CGT	GGA	CGG	CGA	CAA	CCT	ATC	195
30	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGC	AGG	GCC	TGG	GCC	234
	CCC	GGG	CAT	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCC	312
	CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	CCC	429
	CTA	GGG	GGC	GCT	GCC	AGA	GCC	TTG	GCG	CAT	GGC	GTC	468
35	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	507

o

CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG CTG	546
TCC TGC TTG ACC ATC CCA GCT TCC GCT	573

(2) INFORMATION FOR SEQ ID NO: 111:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 10 (C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
15 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG	234
CCC GGG TAC CCT TGG CCC CTC TAT GGC AAC GAG GGC TTG	273
GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCC CGG	312
CCT AGT TGG GGC CCC ACC GAC CCC CGG CGT AGG TCG CGT	351
AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC	429
20 CTA GGG GGT GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
GTT CTG GAG GAC GGC GTG AAT TAT GCA ACA GGG AAT TTG	507
CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT TTG CTG	546
TCC TGT TTG ACC ATC CCA GCT TCC GCT	573

(2) INFORMATION FOR SEQ ID NO: 112:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 30 (C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156

35

°

	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGC	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAC	GAG	GGC	ATG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCC	CGG	312
	CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
5	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
	CTA	GGG	GGC	GCT	GCC	AGG	GCC	TTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
	TCC	TGT	TTG	ACC	ATT	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 113:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P10

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

20

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAC	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGC	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TTG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
25	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
	CTA	GGG	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	CTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
	TCC	TGC	CTG	ACC	ATC	CCA	GCG	TCC	GCT					573

30

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

5	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGG CCC GAG GGC AGG GCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG	312
10	CCT AGT TGG GGC CCC AAC GAC CCC CGG CGT AGG TCG CGT	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC	429
	CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAC TAC GCA ACA GGG AAT TTG	507
	CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG TTG	546
	TCC TGT TTG ACC ATC CCA GCT TCC GCC	573

(2) INFORMATION FOR SEQ ID NO: 115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

25	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAG CCT ATC	195
	CCC AAG GCT CGC CAG CCC GAG GGC AGG GCC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGT GGC TCC CGG	312
	CCT AGT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT	351
30	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC	390
	GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC	429
	CTA GGG GGC GCT GCC AGG GCT CTG GCA CAT GGT GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT TTG	507
	CCC GGT TGC TCT TTT TCT ATC TTC CTC TTG GCT CTG CTG	546
	TCT TGT CTG ACC ATC CCA GCT TCC GCT	573

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGC	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	CGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CAG	CCC	GAG	GGC	AGG	GCC	TGG	GCT	CAG	234
CCT	GGG	TAC	CCC	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	ATG	273
GGA	TGG	GCA	GGA	TGG	CTC	CTG	TCC	CCC	CGC	GGC	TCT	CGG	312
CCT	AGT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
CTA	GGG	GGC	GCT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
GTG	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	CTG	507
CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
TCC	TGT	CTG	ACC	ATC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGC	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGT	AGG	GCC	TGG	GCT	CAG	234

°
 CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGT TCT CGG 312
 CCT AGT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAA GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGC GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 5 CTC CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAC TTG 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTA GCT TTG CTA 546
 TCC TGT TTG ACC ATC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 10
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8
 15
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGC CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
 TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC 195
 20 CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG 234
 CCC GGG CAC CCT TGG CCC CTC TAT GGC AAT GAG GGC TTG 273
 GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG 312
 CCT AGT TGG GGC CCC ACA GAC CCC CGG CGT AGG TCG CGT 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCC CCC 429
 CTA GGG GGT GCT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
 GTC CTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAC TTG 507
 25 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTA 546
 TCC TGT TTG ACC GTC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S9
 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTC	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
5	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCA	ACT	AGG	AAG	ACT	156
	TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CAT	CCC	GAG	GGC	AGG	GCC	TGG	GCT	CAG	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAC	GGC	AAT	GAG	GGC	TTG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	CGG	312
	CCT	AGT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCC	CCC	429
10	CTA	GGG	GGC	GCT	GCC	AGG	GCT	CTG	GCG	CAT	GGC	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAC	CTC	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTG	GCT	TTG	CTG		546
	TCC	TGT	TTG	ACC	ATC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 120:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
25	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACC	AGG	AAG	ACT	156
	TCA	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
	CCC	AAG	GCT	CGC	CAA	CCC	GAG	GGC	AGG	ACC	TGG	GCT	CAG	234
	CCC	GGG	TAT	CCT	TGG	CCC	CTC	TAT	GGC	AAC	GAG	GGC	ATG	273
	GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCT	CGG	312
	CCT	AAT	TGG	GGC	CCC	ACG	GAC	CCC	CGG	CGT	AGG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGT	GCC	CCC	429
30	CTA	GGG	GGC	GTT	GCC	AGA	GCC	TTG	GCA	CAT	GGT	GTC	CGG	468
	GTT	CTG	GAG	GAC	GGC	GTG	AAC	TAT	GCA	ACA	GGG	AAT	TTA	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTG	GCT	TTG	CTG		546
	TCC	TGC	TTG	ACC	ACC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 121:

35

o

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
10	GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACC AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CGA CCC GAG GGC ACC TGG GCT CAG	234
	CCC GGG TAT CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
	GGG TGG GCA GGA TGG CTC CTG TCA CCC CAT GGC TCT CGG	312
15	CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGT	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGC TTC	390
	GCC GAC CTC ATG GGC TAC ATC CCG CTC GTC GGC GCC CCC	429
	CTA GGG GGC GTT GCC AGA GCC CTG GCA CAC GGT GTC CGG	468
	GTT CTG GAG GAC GGC GTG AAC TAC GCA ACA GGG AAT ATA	507
	CCC GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTG	546
	TCC TGT CTG ACC ACC CCA GTT TCC GCT	573

20

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAG ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC	78
30	GGT GGC CAG ATC GTC GGT GGA GTT TAC CTG TTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCC GAG CGG TCG CAA CCT CGT GGA AGG CGA CAA CCT ATC	195
	CCC AAG GCT CGC CAA CCC GAG GGC ACC TGG GCT CAG	234
	CCC GGG TAC CCT TGG CCC CTC TAT GGC AAT GAG GGC ATG	273
35	GGG TGG GCA GGA TGG CTC CTG TCA CCC CGC GGC TCT CGG	312

0
CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC 351
AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GCC CCC 429
TTA GGG GGC GTT GCC AGA GCC CTG GCA CAT GGT GTC CGG 468
GTT GTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT TTG 507
CCC GGT TGC TCT TTC TCT ATC TTC CTC TTG GCT CTG CTG 546
5 TCC TGT TTG ACC ATC CCA GCT TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
10 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

15 ATG AGC ACG ACT CCT AAA CCT CAA AGA AAA ACC AAA CGT 39
AAC ACC AGC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC 78
GGT GGT CAG ATC GTT GGT GGA GTT TAC CTG TTG CCG CGC 117
AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT AGG AAG ACT 156
TCC GAG CGA TCG CAA CCT CGT GGC AGG CGA CAA CCT ATC 195
CCC AAG GCT CGC CGG CCC GAG GGT AGG GCC TGG GCT CAG 234
CCC GGG CAC CCT TGG CCC CTC TAT GCC AAT GAG GGC TTG 273
20 GGG TGG GCG GGA TGG CTC CTG TCA CCC CGC GGC TCC CGG 312
CCT AGT TGG GGC CCC ACG GAC CCC CGG CGT AGG TCG CGC 351
AAT TTG GGT AAG GTC ATC GAT ACC CTC ACA TGC GGC TTC 390
GCC GAC CTC ATG GGG TAC ATT CCG CTC GTC GGC GGC CCC 429
CTA GGG GGC GTT GCC AGG GCC CTG GCG CAT GGC GTC CGG 468
GTT GTG GAG GAC GGC GTG AAC TAT GCA ACA GGG AAT CTG 507
CCT GGT TGC TCT TTC TCT ATC TTC CTT TTG GCT TTG CTG 546
25 TCT TGT CTG ACC ATC CCA GCT TCC GCT 573

30

35

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	CTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	ACT	156
TCC	GAG	CGG	TCG	CAA	CCT	CGT	GGA	AGG	CGA	CAA	CCT	ATC	195
CCC	AAG	GCT	CGC	CGG	CCC	GAG	GGT	AGG	GCC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	GAC	GAG	GGC	ATG	273
GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCA	CCC	CGC	GGC	TCC	CGG	312
CCT	AAT	TGG	GGC	CCC	ACA	GAC	CCC	CGG	CGT	AGG	TCG	CGT	351
AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACA	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATT	CCG	CTC	GTC	GGC	GCT	CCC	429
TTA	GGG	GGC	GTT	GCC	AGG	GCC	CTG	GCG	CAT	GGC	GTC	CGG	468
GTT	CTG	GAG	GAC	GGC	GTG	AAT	TAC	GCA	ACA	GGG	AAT	TTG	507
CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	CTC	TTG	GCT	TTG	CTG	546
TCC	TGC	TTG	ACC	ATC	CCA	GCT	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGC	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
TCC	GAG	CGA	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
CCC	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
CCA	GGA	TAT	CCC	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGA	CTC	273

0
 GGC TGG GCA GGA TGG CTC CTG TCC CCC CGA GGT TCC CGT 312
 CCC TCC TGG GGC CCC AAT GAC CCC CGG CAT AGG TCG CGC 351
 AAC GTG GGT AAG GTC ATC GAT ACC CTA ACG TGC AGC CTT 390
 GCC GAC CTC ATG GGG TAC GTC CCC GTC GTA GGC GGC CCG 429
 TTG GGT GGC GTC GCC AGA GCT CTC GCG CAT GGC GTG AGA 468
 GTC CTG GAG GAC GGG GTT AAT TAT GCA ACA GGG AAC TTA 507
 5 CCT GGT TGC TCC TTT TCT ATT TTC CTG GCC CTA CTG 546
 TCC TGC ATC ACC ATT CCA GTC TCC GCT 573

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 10
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US10
 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
 AAC ACT AAC CGT CGC CCA CAA GAC GTT AAG TTT CCG GGC 78
 GGC GGC CAG ATC GTT GGC GGA GTA TAC TTG TTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC GCG ACA AGG AAG ACT 156
 TCG GAG CGG TCC CAG CCA CGT GGG AGG CGC CAG CCC ATC 195
 20 CCC AAA GAT CGG CGC CCC ACT GGC AAG TCC TGG GGA AAA 234
 CCA GGA TAC CCT TGG CCC CTA TAT GGG AAT GAG GGA CTC 273
 GGC TGG GCA GGA TGG CTC CTG TCC CCC CGA GGT TCC CGT 312
 CCC TCT TGG GGC CCC ACT GAT CCC CGG CAT AGG TCG CGC 351
 AAC GTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGC TTT 390
 GCC GAC CTC ATG GGA TAC ATC CCC GTC GTG GGC GCT CCG 429
 CTT GGT GGC GTC GCC AGA GCT CTC GCG CAT GGC GTG AGG 468
 GTC CTG GAG GAC GGG GTT AAT TAT GCA ACA GGG AAC TTA 507
 25 CCC GGT TGC TCC TTT TCT ATC TTC CTG GCC TTA CTG 546
 TCC TGC ATC ACC ATT CCA GTC TCT GCT 573

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9
 35

o

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

	ATG	AGC	ACA	AAT	CCA	AAA	CCC	CAA	AGA	AAA	ACC	ATA	AGA	39
	AAC	ACC	AAC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTT	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	TTG	CCG	CGC	117
5	AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	ACG	ACA	AGG	AAG	ACT	156
	TCG	GAG	CGG	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
	CCC	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAC	CCC	TGG	CCT	CTA	TAT	GGG	AAT	GAG	GGA	CTC	273
	GGC	TGG	GCG	GGA	TGG	CTC	CTG	TCC	CCC	CGA	GGT	TCC	CGT	312
	CCC	TCT	TGG	GGC	CCC	AGT	GAC	CCC	CGG	CAT	AGG	TCG	CGC	351
	AAC	GTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGC	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCC	GTC	GTA	GGC	GCC	CCG	429
10	CTT	GGT	GGC	GTT	GCC	AGA	GCT	CTC	GCG	CAC	GGC	GTG	AGA	468
	GTC	CTG	GAG	GAC	GGG	GTT	AAT	TAT	GCA	ACA	GGG	AAC	CTA	507
	CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTG	GCC	CTA	CTG		546
	TCC	TGC	ATC	ACC	ACT	CCG	GCC	TCT	GCT					573

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

	ATG	AGC	ACA	ATT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACT	AAC	CGT	CGC	CCA	CAA	GAC	GTT	AAG	TTT	CCG	GGC	78
	GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	CTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
25	TCG	GAG	CGG	TCC	CAG	CCT	CGT	GGA	AGG	CGC	CAG	CCC	ATC	195
	CCT	AAA	GAT	CGG	CGC	TCC	ACT	GGC	AAG	TCC	TGG	GGA	AAA	234
	CCA	GGA	TAC	CCC	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGG	CTC	273
	GGC	TGG	GCA	GGA	TGG	CTC	CTG	TCC	CCC	CGA	GGT	TCT	CGT	312
	CCC	TCT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CAT	AGG	TCG	CGC	351
	AAT	GTG	GGT	AAA	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGC	TTT	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCC	GTC	GTA	GGC	GCC	CCG	429
30	CTT	GGT	GGT	GTC	GCC	AGA	GCT	CTT	GCG	CAT	GGC	GTG	AGA	468
	GTC	CTG	GAG	GAC	GGA	GTT	AAT	TAT	GCA	ACA	GGT	AAC	TTA	507
	CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	TTG	CTA	GCC	CTG	CTG	546
	TCC	TGC	ATC	ACT	ATT	CCG	GTT	TCA	GCT					573

(2) INFORMATION FOR SEQ ID NO: 129:

35

0

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

	ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACA AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGT	78
10	GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC	117
	AGG GGC CCT AGG TTG GGT GTG CGC GCG ACA AGG AAG ACT	156
	TCC GAG CGA TCC CAG CCG CGT GGG AGA CGC CAG CCC ATC	195
	CCG AAA GAT CGG CGC TCC ACC GGC AAG TCC TGG GGA AAA	234
	CCA GGA TAT CCT TGG CCT CTT TAC GGA AAC GAG GGC TGC	273
	GGT TGG GCA GGT TGG CTC CTG TCC CCC CGC GGG TCT CGT	312
	CCT ACT TGG GGC CCC ACT GAC CCC CGG CAT AGA TCA CGT	351
15	AAT TTG GGC AGA GTC ATC GAT ACC ATT ACA TGT GGT TTT	390
	GCC GAC CTC ATG GGG TAC ATC CCT GTC GTT GGC GCC CCG	429
	GTC GGA GGC GTC GCC AGA GCT CTG GCA CAT GGT GTT AGG	468
	GTC CTG GAA GAC GGG ATA AAC TAT GCA ACA GGG AAT TTG	507
	CCT GGT TGC TCT TTT TCT ATC TTC TTG CTT GCT CTT CTG	546
	TCA TGC TTC ACA GTG CCA GTG TCT GCA	573

20

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACA AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGT	78
30	GGC GGT CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC	117
	AGG GGC CCC AGG TTG GGT GTG CGC GCG ACA AGG AAG ACT	156
	TCC GAG CGA TCC CAG CCG CGT GGG AGA CGC CAG CCC ATC	195
	CCG AAA GAT CGG CGC TCC ACC GGC AAG TCC TGG GGA AAG	234
	CCA GGA TAT CCT TGG CCT CTG TAC GGA AAC GAG GGC TGC	273
	GGC TGG GCA GGT TGG CTC CTG TCC CCC CGC GGG TCT CGT	312
35	CCT ACT TGG GGC CCC ACT GAC CCC CGG CAC AGA TCA CGT	351

AAC TTG GGC AAG GTC ATC GAT ACC ATT ACG TGT GGT TTT 390
 GCC GAC CTC ATG GGG TAC ATC CCT GTC GTT GGC GCC CCG 429
 GTC GGA GGC GTC GCC AGA GCT CTG GCA CAC GGT GTT AGG 468
 GTC CTG GAA GAC GGG ATA AAT TAC GCA ACA GGG AAT CTG 507
 CCT GGT TGC TCC TTT TCT ATC TTC TTA CTT GCT CTT CTG 546
 TCG TGC GCC ACG GTG CCG GTG TCT GCA 573

5

(2) INFORMATION FOR SEQ ID NO: 131:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK11

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

15 ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
 AAT ACA AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGT 78
 GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC 117
 AGG GGC CCC AGG TTG GGT GTG CGC ACG ACA AGG AAG ACT 156
 TCC GAG CGA TCC CAG CCG CGT GGG AGA CGC CAG CCC ATC 195
 CCG AAA GAT CGG CGC TCC ACC GGC AAG CCC TGG GGA AAG 234
 CCA GGA TAT CCT TGG CCC CTG TAT GGA AAC GAG GGC TGC 273
 20 GGC TGG GCA GGT TGG CTC CTG TCC CCC CGC GGG TCT CAT 312
 CCT AAT TGG GGC CCC ACT GAC CCC CGG CAT AAA TCA CGC 351
 AAT TTG GGT AAA GTC ATC GAC ACC ATT ACG TGT GGT TTT 390
 GCC GAC CTC ATG GGG TAC ATC CCT GTC GTC GGC GCC CCG 429
 GTC GGA GGC GTC GCC AGA GCT CTG GCA CAC GGT GTT AGA 468
 GTC CTG GAA GAC GGG ATA AAT TAC GCA ACA GGG AAT CTG 507
 CCT GGT TGC TCT TTT TCT ATC TTC TTA CTT GCT CTT CTG 546
 25 TCA TGC TGC ACA GTG CCA GTG TCT GCG 573

25

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW3

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

35

5
 10
 15
 20
 25
 30

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAT	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	ACT	156
TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGA	CGC	CAG	CCC	ATC	195
CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAG	234
CCA	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CAT	312
CCT	AAT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGC	351
AAT	TTG	GGC	AAA	GTC	ATC	GAC	ACC	ATT	ACG	TGT	GGT	TTT	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
GTC	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGA	468
GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	CTG	507
CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTA	CTT	GCT	CTT	CTG	546
TCG	TGC	TTC	ACA	GTG	CCA	GTG	TCT	GCG					573

(2) INFORMATION FOR SEQ ID NO: 133:

15
 20
 25
 30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACA	AAC	CGC	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	CTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACA	AGG	AAG	TCT	156
TCC	GAG	CGA	TCC	CAG	CCG	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
CCG	AAA	GAT	CGG	CGC	TCC	ACC	GGC	AAG	TCC	TGG	GGA	AAG	234
CCG	GGA	TAT	CCT	TGG	CCC	CTG	TAT	GGA	AAC	GAG	GGC	TGC	273
GGC	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGG	TCT	CGT	312
CCT	ACT	TGG	GGC	CCC	ACT	GAC	CCC	CGG	CAT	AGA	TCA	CGC	351
AAT	TTG	GGC	AAA	GTC	ATC	GAC	ACC	ATT	ACG	TGT	GGT	TTT	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCT	GTC	GTT	GGC	GCC	CCG	429
GTT	GGA	GGC	GTC	GCC	AGA	GCT	CTG	GCA	CAC	GGT	GTT	AGG	468
GTC	CTG	GAA	GAC	GGG	ATA	AAT	TAC	GCA	ACA	GGG	AAT	TTG	507
CCT	GGT	TGC	TCT	TTT	TCT	ATC	TTC	TTG	CTT	GCT	CTT	CTG	546
TCG	TGC	TGC	ACA	GTG	CCA	GTG	TCT	GCG					573

(2) INFORMATION FOR SEQ ID NO: 134:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

o

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S83

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

ATG	AGC	ACA	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACT	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTA	TAC	TTG	CTG	CCG	CGC	117
AGG	GGC	CCG	AGA	TTG	GGT	GTG	CGC	GCG	ACG	AGG	AAA	ACT	156
TCC	GAA	CGG	TCC	CAG	CCA	CGT	GGG	AGG	CGC	CAG	CCC	ATC	195
CCT	AAA	GAT	CGG	CGC	ACC	ACT	GGC	AAG	TCC	TGG	GGA	AGG	234
CCA	GGA	TAC	CCT	TGG	CCC	CTG	TAT	GGG	AAT	GAG	GGC	CTC	273
GGC	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCC	CGC	GGT	TCT	CGC	312
CCT	TCA	TGG	GGC	CCC	ACC	GAC	CCC	CGG	CAT	AAA	TCG	CGC	351
AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGT	TTT	390
GCC	GAC	CTC	ATG	GGG	TAC	ATA	CCC	GTC	GTT	GGC	GCT	CCC	429
GTT	GGC	GGC	GTT	GCC	AGA	GCC	CTC	GCC	CAT	GGG	GTG	AGG	468
GTT	CTG	GAG	GAC	GGG	ATA	AAT	TAT	GCA	ACG	GGG	AAT	TTG	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	CTC	TTG	GCC	CTC	TTG	546
TCT	TGC	ATC	TCT	GTG	CCA	GTT	TCC	GCC					573

(2) INFORMATION FOR SEQ ID NO: 135:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK10

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

ATG	AGC	ACA	CTT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACC	ATC	CGT	CGC	CCA	CAG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGC	GGA	CAG	ATC	GTT	GGT	GGA	GTA	TAC	GTG	TTG	CCG	CGC	117
AGG	GGC	CCA	CGA	TTG	GGT	GTG	CGC	GCG	ACG	CGT	AAA	ACT	156
TCT	GAA	CGG	TCG	CAG	CCT	CGC	GGA	CGA	CGA	CAG	CCT	ATC	195
CCC	AAG	CGG	CGT	CGG	AGC	GAA	GGC	CGG	TCC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGT	AAC	GAG	GGC	TGC	273
GGG	TGG	GCA	GGA	TGG	CTC	CTG	TCC	CCA	CGC	GGC	TCC	CGT	312
CCA	TCT	TGG	GGC	GCA	AAC	GAC	CCC	CGG	CGA	CGC	TCC	CGC	351
AAT	TTG	GGT	AAA	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGA	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	429

35

o

GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTC	GCG	CAT	GGC	GTG	AGG	468
GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTC	GCA	ACA	GGG	AAC	TTG	507
CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTT	CTT	GCT	CTG	TTC	546
TCT	TGC	TTA	ATT	CAT	CCA	GCA	GCT	AGT					573

5 (2) INFORMATION FOR SEQ ID NO: 136:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

ATG	AGC	ACA	CTT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACC	ATC	CGT	CGC	CCA	GAC	GTT	AAG	TTC	CCG	GGT		78
GGC	GGA	CAG	ATC	GTT	GGT	GGA	GTA	TAC	GTG	TTG	CCG	CGC	117
AGG	GGC	CCA	CGA	TTG	GGT	GTG	CGC	GCG	ACG	CGT	AAA	ACT	156
TCT	GAA	CGG	TCA	CAG	CCT	CGC	GGA	CGA	CGA	CAG	CCT	ATC	195
CCC	AAG	GCG	CGT	CGG	AGC	GAA	GGC	CGG	TCC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGT	AAT	GAG	GGC	TGC	273
GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCA	CGC	GGC	TCC	CGT	312
CCA	TCT	TGG	GGC	CCA	AAC	GAC	CCC	CGG	CGG	AGG	TCC	CGC	351
AAT	TTG	GGT	AAA	GTC	ATC	GAT	ACC	CTT	ACG	TGC	GGA	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTC	GGC	GCT	CCC	429
GTA	GGA	GGC	GTC	GCA	AGA	GCC	CTC	GCG	CAT	GGC	GTG	AGG	468
GCC	CTT	GAA	GAC	GGG	ATA	AAT	TTT	GCA	ACA	GGG	AAC	TTG	507
CCC	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTT	GCT	CTG	TTC		546
TCC	TGC	TTA	GTT	CAT	CCT	GCA	GCT	AGT					573

25 (2) INFORMATION FOR SEQ ID NO: 137:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

ATG	AGC	ACA	CTT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

35

0
AAC ACC ATC CGT CGC CCA CAG GAC ATC AAG TTC CCG GGT 78
GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC 117
AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT 156
TCT GAA CGG TCA CAG CCT CGC GGA CGG CGA CAG CCT ATC 195
CCC AAG GCG CGT CGG AGC GAA GGC CGA TCC TGG GCT CAG 234
CCC GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC 273
GGG TGG GCA GGG TGG CTC CTG TCC CCA CGC GGC TCC CGT 312
5 CCA TCT TGG GGC CCA AAT GAC CCC CGG CGG AGG TCC CGC 351
AAT TTG GGT AAA GTC ATC GAT ACC CTT ACG TGC GGC TTC 390
GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCC 429
GTA GGA GGC GTC GCA AGA GCC CTC GCG CAT GGC GTG AGG 468
GCC CTT GAA GAC GGG ATA AAT TTT GCA ACA GGG AAC TTG 507
CCC GGT TGC TCT TTT TCT ATC TTC CTT CTT GCC CTG TTC 546
TCT TGC TTA ATT CAT CCA GCA GCT AGT 573

10

(2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK12

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

20 ATG AGC ACA CTT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
AAC ACC ATC CGT CGC CCA CAG GAC GTC AAG TTC CCG GGT 78
GGC GGA CAG ATC GTT GGT GGA GTA TAC GTG TTG CCG CGC 117
AGG GGC CCA CGA TTG GGT GTG CGC GCG ACG CGT AAA ACT 156
TCT GAA CGG TCA CAG CCT CGC GGA CGG CGA CAG CCT ATC 195
CCC AAG GCG CGT CGG AGC GAA GGC CGG TCC TGG GCT CAG 234
CCT GGG TAC CCT TGG CCC CTC TAT GGT AAC GAG GGC TGC 273
GGG TGG GCA GGG TGG CTC CTG TCC CCA CGC GGC TCC CGT 312
25 CCA TCT TGG GGC CCA AAC GAC CCC CGG CGG AGG TCC CGC 351
AAT TTG GGT AAG GTC ATC GAT ACC CTC ACG TGC GGA TTC 390
GCC GAC CTC ATG GGG TAC ATC CCG CTC GTC GGC GCT CCT 429
GTA GGG GGC GTC GCA AGA GCC CTC GCG CAT GGC GTG AGG 468
GCC CTT GAA GAC GGG ATA AAT TTC GCA ACA GGG AAC TTG 507
CCC GGT TGC TCC TTT TCT ATC TTC CTT CTT GCT CTG TTC 546
TCT TGC CTA ATT CAT CCA GCA GCT AGT 573

30

(2) INFORMATION FOR SEQ ID NO: 139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

35

0

(D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z4

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCC	ATG	GAC	GTA	AAG	TTC	CCG	GGT	78
GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGA	AAG	ACT	156
TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGC	AGG	CGT	CAA	CCT	ATC	195
CCC	AAG	GCG	CGC	CAG	CCA	GAG	GGC	AGA	TCC	TGG	GCG	CAG	234
CCC	GGG	TAC	CCT	TGG	CCC	CTC	TAT	GGC	AAT	GAG	GGC	TGC	273
GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCT	CCT	CGC	GGC	TCT	CGG	312
CCA	TCT	TGG	GGC	CCA	AAT	GAT	CCC	CGG	CGG	AGA	TCG	CGC	351
AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTG	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	ATC	GTG	GGC	GCC	CCC	429
GTG	GGG	GGC	GTC	CGC	AGG	GCT	CTG	GCG	CAT	GGC	GTC	AGG	468
GCT	GTG	GAG	GAC	GGG	ATT	AAC	TAT	GCA	ACA	GGG	AAT	CTT	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTT	TTG	GCA	CTT	CTT	546
TCG	TGC	CTC	ACT	GTT	CCA	GCG	TCG	GCT					573

(2) INFORMATION FOR SEQ ID NO: 140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z8

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCC	ATG	GAT	GTA	AAA	TTC	CCA	GGC	78
GGC	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGC	AGG	CGT	CAG	CCT	ATC	195
CCC	AAG	GCA	CGT	CGG	TCC	GAG	GGT	AGG	TCC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCA	TGG	CCT	CTT	TAC	GGT	AAT	GAA	GGC	TGT	273
GGG	TGG	GCA	GGT	TGG	CTC	CTG	TCC	CCC	CGC	GGC	TCT	CGA	312
CCG	TCT	TGG	GGC	CCA	AAT	GAT	CCC	CGG	CGG	AGG	TCG	CGC	351
AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTC	ACG	TGC	GGC	TTC	390
GCC	GAC	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTG	GGC	GCC	CCA	429
GTA	GGA	GGC	GTC	GCC	AGA	GCC	CTG	GCG	CAT	GGC	GTC	AGG	468
GCT	GTG	GAG	GAC	GGG	ATC	AAC	TAT	GCA	ACA	GGG	AAC	CTT	507

35

o

CCT GGT TGC TCT TTC TCT ATC TTC CTC TTG GCA CTT CTC	546
TCG TGC CTA ACC GTC CCA GCG TCT GCT	573

(2) INFORMATION FOR SEQ ID NO: 141:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 10 (C) INDIVIDUAL ISOLATE: Z1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

ATG AGC ACA AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
AAC ACC AAC CGT CGC CCC ATG GAT GTG AAA TTC CCG GGC	78
GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG CTG CCG CGC	117
AGG GGC CCC CGG TTG GGT GTG CGC GCA GCT CGG AAG ACT	156
15 TCG GAG CGG TCA CAA CCT CGT GGC AGG CGT CAG CCT ATC	195
CCC AAG GCG CGC CGG TCC GAG GGC AGG TCC TGG GCT CAG	234
CCC GGC TAC CCT TGG CCC CTT TAC GGC AAT GAG GGC TGT	273
GGG TGG GCA GGG TGG CTC CTG TCC CCC CGC GGT TCC AGG	312
CCG TCT TGG GGC CCC AAT GAT CCC CGG CGT AGG TCC CGT	351
AAT CTG GGT AAA GTC ATC GAT ACC CTG ACG TGT GGC TTC	390
GCC GAC CTC ATG GGA TAC ATT CCG CTC GTA GGC GCC CCT	429
20 GTG GGT GGC GTC GCC AGG GCC CTG GCG CAT GGC GTC AGG	468
GCC GTG GAG GAC GGA ATT AAC TAC GCA ACA GGG AAC CTT	507
CCT GGT TGC TCT TTC TCT ATC TTT CTT CTT GCA CTT CTC	546
TCG TGC CTG ACA ACA CCA GCA TCT GCC	573

(2) INFORMATION FOR SEQ ID NO: 142:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 30 (C) INDIVIDUAL ISOLATE: Z5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
AAC ACC AAC CGC CGC CCC ATG GAT GTA AAA TTC CCG GGT	78
GGT GGT CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC	117
AGG GGC CCC AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT	156

35

°

TCG	GAG	CGG	TCG	CAA	CCT	CGC	GGC	AGG	CGT	CAG	CCT	ATC	195
CCC	CAG	GCA	CGT	CGG	TCC	GAG	GGC	AGG	TCC	TGG	GCT	CAG	234
CCC	GGG	TAC	CCT	TGG	CCT	CTT	TAT	GGC	AAT	GAG	GGC	TGT	273
GGG	TGG	GCA	GGG	TGG	CTC	CTG	TCC	CCC	CGC	GGA	TCT	CGG	312
CCA	TCT	TGG	GGC	CAA	AAT	GAT	CCC	CGG	CGT	AGG	TCC	CGC	351
AAT	CTG	GGT	AAG	GTC	ATC	GAT	ACC	CTG	ACG	TGT	GGC	TTC	390
GCC	GAC	CTC	ATG	GGA	TAC	ATT	CCG	CTC	GTC	GGC	CCA		429
5	GTA	GGT	GGC	GTC	GCC	AGG	GCC	TTG	GCG	CAT	GGC	GTC	468
GCC	CTG	GAG	GAC	GGA	ATC	AAC	TAT	GCA	ACA	GGG	AAT	CTT	507
CCT	GGT	TGC	TCC	TTT	TCT	ATC	TTC	CTA	CTT	GCA	CTT	TTC	546
TCG	TGC	TTG	ACA	ACA	CCG	GCA	TCC	GCT					573

(2) INFORMATION FOR SEQ ID NO: 143:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 15 (C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	CGT	39
AAC	ACC	AAC	CGC	CGC	CCC	ATG	GAC	GTT	AAG	TTC	CCG	GGT	78
GGT	GGC	CAG	ATC	GTT	GGC	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
20	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	AGG	AAG	156
TCG	GAG	CGG	TCG	CAA	CCT	CGT	GGG	AGA	CGC	CAG	CCT	ATC	195
CCC	AAG	GCA	CGT	CGA	TCT	GAG	GGA	AGG	TCC	TGG	GCT	CAG	234
CCC	GGG	TAT	CCA	TGG	CCT	CTT	TAC	GGT	AAT	GAG	GGT	TGC	273
GGG	TGG	GCG	GGA	TGG	CTC	CTG	TCA	CCC	CGT	GGC	TCT	CGA	312
CCG	TCT	TGG	GGT	CCA	AAT	GAT	CCC	CGG	CGA	AGG	TCC	CGC	351
AAC	TTG	GGT	AAG	GTC	ATC	GAT	ACT	CTA	ACT	TGC	GGT	TTC	390
GCC	GAT	CTC	ATG	GGA	TAC	ATC	CCG	CTC	GTA	GGC	GCC	CCC	429
25	GTG	GGC	GGC	GTC	GCC	AGG	GCC	CTG	GCA	CAT	GGT	GTT	468
GCT	GTG	GAG	GAC	GGG	ATC	AAT	TAT	GCA	ACA	GGG	AAT	CTT	507
CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTC	CTC	TTG	GCA	CTT	CTT	546
TCG	TGC	CTA	ACT	GTT	CCC	ACC	TCG	GCC					573

(2) INFORMATION FOR SEQ ID NO: 144:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vi) ORIGINAL SOURCE:

35

o

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCC ATG GAC GTT AAG TTC CCG GGC	78
5	GGT GGC CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCC AGA TTG GGT GTG CGC ACA ACT AGG AAG ACT	156
	TCG GAG CGG TCG CAA CCT CGT GGG AGA CGT CAG CCT ATC	195
	CCC AAG GCA CGT CGA TCT GAG GGA AGG TCC TGG GCT CAA	234
	CCC GGG TAC CCA TGG CCT CTT TAC GGT AAC GAG GGT TGC	273
	GGG TGG GCA GGA TGG CTC TTG TCA CCC CGT GGC TCT CGA	312
	CCG TCT TGG GGC CCA AAT GAT CCC CGG CGA AGG TCC CGC	351
10	AAC TTG GGT AAG GTC ATC GAT ACC CTA ACC TGC GGC TTT	390
	GCC GAC CTC ATG GGA TAC ATC CCG CTC GTA GGC GCC CCC	429
	GTG GGC GGC GTC GCC AGG GCC CTA GCG CAT GGC GTT AGG	468
	GCT CTG GAG GAC GGG ATT AAT TAT GCA ACA GGG AAC CTT	507
	CCC GGT TGC TCT TTT TCT ATC TTC CTG GCA CTT CTT	546
	TCG TGC CTG ACT GTT CCC GCC TCG GCC	573

15 (2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA CGT	39
	AAC ACC AAC CGC CGC CCA ATG GAC GTT AAG TTC CCG GGT	78
25	GGC GGC CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGA TTG GGT GTG CGC GCG ACT AGG AAG ACT	156
	TCG GAG CGG TCG CAA CCT CGT GGG AGG CGC CAG CCT ATC	195
	CCC AAG GCG CGC CAA CTC GAG GGT AGG TCC TGG GCT CAG	234
	CCT GGG TAT CCT TGG CCC CTT TAC GGC AAT GAG GGC TGC	273
	GGG TGG GCG GGA TGG CTC CTG TCA CCC CGT GGC TCT CGG	312
	CCG TCT TGG GGC CCG AAT GAT CCC CGG CGG AGG TCC CGC	351
30	AAC TTG GGT AAG GTC ATC GAT ACC CTA ACT TGC GGC TTC	390
	GCC GAC CTC ATG GGA TAC ATC CCG GTC GTA GGC GCC CCC	429
	GTG GGT GGC GTC GCC AGA GCC CTG GCG CAT GGC GTC AGG	468
	CTT CTG GAG GAC GGG GTC AAT TAT GCA ACA GGG AAT CTT	507
	CCC GGT TGC TCT TTT TCT ATC TTC CTG GCA CTG CTC	546
	TCG TGC CTG ACT GTT CCC GCT TCG GCC	573

35

(2) INFORMATION FOR SEQ ID NO: 146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

10	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTT AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTC TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT	195
	CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA	234
15	CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC	273
	GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312
	CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAG TCG CGC	351
	AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	429
	GTT GGG GGC GTC GCA AGG GCC CTT GCA CAT GGT GTG AGG	468
	GTT CTT GAG GAC GGG GTA AAC TAT GCA ACG GGG AAT TTG	507
20	CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC	546
	TCG TGC CTG ACC GTC CCG GCC TCT GCA	573

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

30	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGA TTG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT	195
35	CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA	234

CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC 273
 GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG 312
 CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAA TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGC GGA TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC 429
 GTT GGG GGC GTC GCA AGG GCC CTC GCA CAT GGT GTG AGG 468
 GTT CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTG 507
 5 CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC 546
 TCG TGC TTG ACC GTC CCA GCC TCT GCA 573

(2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 10
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA7
 15
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA 39
 AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC 78
 GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCT AGG TTG GGT GTG CGC GCG ACT CGG AAG ACT 156
 TCA GAA CGG TCG CAA CCC CGT GGG CGG CGC CAG CCT ATT 195
 20 CCC AAG GCG CGC CAA CCC ACG GGC CGG TCC TGG GGT CAA 234
 CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC 273
 GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG 312
 CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAG TCG CGC 351
 AAT TTG GGT AAG GTC ATC GAC ACC CTA ACA TGC GGA TTC 390
 GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC 429
 GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG 468
 GTT CTT GAG GAC GGG GTA AAT TAC GCA ACA GGG AAT CTG 507
 25 CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTC 546
 TCG TGC CTG ACC TCG CCA GCC TCC GCA 573

(2) INFORMATION FOR SEQ ID NO: 149:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA1

o

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CTC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
5	TCG	GAA	CGG	TCG	CAA	CCC	CGT	GGG	CGG	CGC	CAG	CCT	ATT	195
	CCC	AAG	GCG	CGC	CAA	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAC	GCC	AAT	GAG	GGC	CTC	273
	GGG	TGG	GCA	GGG	TGG	TTG	CTC	TCC	CCC	CGA	GGC	TCT	CGG	312
	CCT	AAT	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGG	AAG	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
	GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
	GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	468
10	GTT	CTT	GAG	GAC	GGG	GTA	AAC	TAC	GCA	ACA	GGG	AAT	TTG	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	ATC	CTT	GCA	CTT	CTT	546
	TCC	TGT	CTG	ATC	ATC	CCG	GCC	TCT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 150:

15	(i)	SEQUENCE CHARACTERISTICS:
		(A) LENGTH: 573 base pairs
		(B) TYPE: nucleic acid
		(C) STRANDEDNESS: single
		(D) TOPOLOGY: linear
	(vi)	ORIGINAL SOURCE:
		(A) ORGANISM: homosapiens
20		(C) INDIVIDUAL ISOLATE: SA3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

	ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
	AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
	GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
	AGG	GGC	CCC	AGG	TTG	GGT	GTG	CGC	GCG	ACT	CGG	AAG	ACT	156
25	TCA	GAA	CGG	TCG	CAA	CCC	CGT	GGA	CGG	CGC	CAG	CCT	ATT	195
	CCC	AAG	GCT	CGC	CAG	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
	CCC	GGG	TAC	CCT	TGG	CCC	CTT	TAC	GCC	AAT	GAG	GGC	CTC	273
	GAG	TGG	GCA	GGG	TGG	TTG	CTC	TCC	CCC	CGA	GGC	TCT	CGG	312
	CCT	AGT	TGG	GGC	CCC	AAC	GAC	CCC	CGG	CGG	AAA	TCG	CGC	351
	AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
	GCC	GAT	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
	GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAT	GGT	GTG	AGG	468
30	GTT	CTT	GAG	GAC	GGG	GTA	AAC	TAC	GCA	ACA	GGG	AAT	TTA	507
	CCC	GGT	TGC	TCT	TTC	TCT	ATC	TTT	ATC	CTT	GCA	CTT	CTT	546
	TCA	TGC	CTG	ACC	GTC	CCG	GCC	TCT	GCA					573

(2) INFORMATION FOR SEQ ID NO: 151:

35

o

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC AAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
10	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT AGG TTG GGT GTG CGC GCA ACT CGG AAG ACT	156
	TCA GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT ATC	195
	CCC AAG GCG CGC CAG CCC ACG GGC CGG TCC TGG GGT CAA	234
	CCC GGG TAC CCT TGG CCC CTT TAT GCC AAT GAG GGC CTC	273
	GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312
	CCT AAT TGG GGC CCC AAT GAC CCC CGG CGG AAA TCG CGC	351
15	AAC TTG GGT AAG GTC ATC GAT ACC CTG ACG TGC GGA TTC	390
	GCC GAC CTC ATG GGG TAC ATC CCG CTC GTA GGC GGC CCC	429
	GTT GGG GGC GTC GCA AGG GCT CTC GCA CAC GGT GTG AGG	468
	GTC CTT GAG GAC GGG GTA AAC TAT GCA ACA GGG AAT TTA	507
	CCC GGT TGC TCT TTC TCT ATC TTT ATC CTT GCA CTT CTT	546
	TCA TGC CTG ACT GTC CCG ACC TCT GCC	573

20

(2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

25

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

	ATG AGC ACG AAT CCT AAA CCT CAA AGA AAA ACC CAA AGA	39
	AAC ACC AAC CGC CGC CCA CAG GAC GTC AAG TTC CCG GGC	78
30	GGT GGT CAG ATC GTT GGT GGA GTT TAC TTG TTG CCG CGC	117
	AGG GGC CCT CGT ATG GGT GTG CGC GCG ACT CGG AAG ACT	156
	TCG GAA CGG TCG CAA CCC CGT GGA CGG CGT CAG CCT ATT	195
	CCC AAG GCG CGC CAA TCC GCG GGT CGG TCC TGG GGT CAA	234
	CCC GGG TAC CCT TGG CCC CTT TAC GCC AAT GAG GGC CTC	273
	GGG TGG GCA GGG TGG TTG CTC TCC CCC CGA GGC TCT CGG	312
35	CCT AAT TGG GGC CCC AAT GAC CCC CGG CGA AAA TCG CGC	351

o

AAT	TTG	GGT	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
GTT	GGG	GGC	GTC	GCA	AGG	GCT	CTC	GCA	CAC	GGT	GTG	AGG	468
GTT	CTT	GAG	GAC	GGG	GTA	AAC	TAT	GCA	ACA	GGG	AAT	TTG	507
CCC	GGT	TGC	TCT	TTT	TCT	ATC	TTT	GTC	CTT	GCA	CTT	CTC	546
TCG	TGC	CTA	ACC	GTC	CCT	GCC	TCT	GCA					573

5

(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SAll

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

ATG	AGC	ACG	AAT	CCT	AAA	CCT	CAA	AGA	AAA	ACC	AAA	AGA	39
AAC	ACC	AAC	CGC	CGC	CCA	CAG	GAC	GTC	AAG	TTC	CCG	GGC	78
GGT	GGT	CAG	ATC	GTT	GGT	GGA	GTT	TAC	TTG	TTG	CCG	CGC	117
AGG	GGC	CCT	AGG	TTG	GGT	GTG	CGC	CGC	ACT	CGG	AAG	ACT	156
TCA	GAA	CGG	TCG	CAA	CCC	CGT	GGG	CGG	CGT	CAG	CCT	ATT	195
CCC	AAG	GCG	CGC	CAA	CCC	ACG	GGC	CGG	TCC	TGG	GGT	CAA	234
CCC	GGG	TAC	CCT	TGG	CCC	TTT	TAC	GCC	AAT	GAG	GGC	CTC	273
GGG	TGG	GCA	GGG	TGG	CTG	CTC	TCC	CCT	CGA	GGC	TCT	CGG	312
CCT	AAC	TGG	GGC	CCC	AAT	GAC	CCC	CGG	CGA	AGA	TCG	CGC	351
AAT	TTG	GGC	AAG	GTC	ATC	GAT	ACC	CTA	ACG	TGC	GGA	TTC	390
GCC	GAC	CTC	ATG	GGG	TAC	ATC	CCG	CTC	GTA	GGC	GGC	CCC	429
GTT	GGG	GGC	GTC	GCA	AGG	GCC	CTC	GCA	CAC	GGT	GTG	AGA	468
GCT	CTT	GAG	GAC	GGG	GTA	AAT	TAT	GCA	ACA	GGG	AAT	CTT	507
CCC	GGT	TGC	TCT	TTT	TCC	ATC	TTT	ATC	CTT	GCA	CTT	CTC	546
TCG	TGC	TTG	ACC	GTC	CCG	GCC	ACT	GCA					573

25

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

ATG	AGC	ACA	CTT	CCA	AAA	CCC	CAA	AGA	AAA	ACC	AAA	AGA	39
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

35

AAC ACC AAC CGT CGC CCA ACG GAC GTC AAG TTC CCG GGT 78
 GGC GGT CAG ATC GTT GGC GGA GTT TAC TTG TTG CCG CGC 117
 AGG GGC CCC CGG TTG GGT GTG CGC GCG ACG AGA AAG ACT 156
 TCC GAG CGA TCC CAG CCC AGA GGC AGG CGC CAA CCT ATA 195
 CCA AAG GCG CGC CAG CCC CAG GGC AGG CAC TGG GCT CAG 234
 CCC GGA TAC CCT TGG CCT CTT TAT GGA AAC GAG GGC TGT 273
 GGG TGG GCA GGT TGG CTC CTG TCC CCC CGC GGC TCC CGG 312
 CCA CAT TGG GGC CCC AAT GAC CCC CGG CGT CGA TCC CGG 351
 AAT TTG GGT AAG GTC ATC GAT ACC CTA ACG TGT GGG TTC 390
 GCC GAT CTC ATG GGG TAC ATT CCC GTC GTG GGC GCG CCT 429
 TTG GGC GGC GTC GCG GCT GCG CTC GCA CAT GGC GTG AGG 468
 GCA ATC GAG GAC GGG ATC AAT TAT GCA ACA GGG AAT CTC 507
 CCC GGT TGC TCT TTC TCT ATC TTC CTT TTG GCA CTA CTC 546
 TCG TGC CTC ACA ACG CCA GCT TCG GCT 573

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Pro Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80 85
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150

o

```

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155                               160                               165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170                               175                               180
Ser Cys Leu Thr Val Pro Ala Ser Ala
185                               190

```

5

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
   1           5           10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
   15           20           25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
   30           35           40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
   45           50           55
20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
   60           65           70
Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
   75           80           85
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
   90           95
25 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
   100          105          110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
   115          120          125
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
   130          135          140
Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
   145          150
30 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
   155          160          165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
   170          175          180
Ser Cys Leu Thr Val Pro Ala Ser Ala
   185          190

```

35

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S14

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				
	Pro	Glu	Gly	Arg	Thr	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	90				95					100				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
	105				110					115				
20	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	120				125					130				
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	135				140					145				
	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
	150				155					160				
25	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	165				170					175				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	180				185					190				
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

o

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SW1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

5 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
10 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
60 65 70
Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75 80
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
100 105 110
15 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140
Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155 160 165
20 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170 175 180
Ser Cys Leu Thr Val Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10

35

5 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 5 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 10 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 15 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 160:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DR4

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 30 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70

o

Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 5 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 10 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 161:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 25 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 30 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125

35

Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 5 Leu Pro Gly Cys Pro Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 162:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 15 (C) INDIVIDUAL ISOLATE: S45

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Met Ser Thr Asn Pro Lys Pro Gln Arg Ala Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro
 75 80
 25 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 30 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180

Ser Cys Leu Thr Ile Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: D1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
15	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30					35					40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50				55		
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
			60					65				70		
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
			75					80						
20	Leu	Tyr	Gly	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
		100				105					110			
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115			120						125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
			130					135					140	
25	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
			145					150						
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170				175						180			
30	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
		185					190							

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
10	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30					35				40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45					50						55		
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60					65						70		
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75					80								
15	Leu	Tyr	Gly	Asn	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Thr	Asp	Pro
	100				105							110		
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	115					120						125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	130					135							140	
20	Gly	Ala	Pro	Leu	Gly	Gly	Ala	Ala	Arg	Ala	Leu	Ala	His	Gly
	145					150								
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170				175							180		
25	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
	185					190								

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: P10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40

5 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 10 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 15 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

25 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 30 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 35 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95

Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 5 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

10

(2) INFORMATION FOR SEQ ID NO: 168:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SW2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

20

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 25 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 30 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150

35

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

5

(2) INFORMATION FOR SEQ ID NO: 169:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

15 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 20 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 25 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
 145 150
 30 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

35

(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: IND8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```

10  Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
    1          5          10
    Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
    15          20          25
    Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
    30          35          40
    Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
    45          50          55
15  Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
    60          65          70
    Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro
    75          80          85
    Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
    90          95
    Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
    100          105          110
20  Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
    115          120          125
    Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
    130          135          140
    Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
    145          150          155
25  Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
    160          165          170
    Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
    175          180
    Ser Cys Leu Thr Val Pro Ala Ser Ala
    185          190
  
```

(2) INFORMATION FOR SEQ ID NO: 171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: S9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

```

5  Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
    1      5      10
  15  Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
    20      25
  30  Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
    35      40
  45  Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
    50      55
  60  Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg His
    65      70
  75  Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly Tyr Pro Trp Pro
    80
  85  Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
    90      95
 100  Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
    105      110
 115  Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
    120      125
 130  Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
    135      140
 145  Gly Ala Pro Leu Gly Gly Ala Ala Arg Ala Leu Ala His Gly
    150
 155  Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
    160      165
 170  Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
    175      180
 185  Ser Cys Leu Thr Ile Pro Ala Ser Ala
    190

```

(2) INFORMATION FOR SEQ ID NO: 172:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: HK3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
  1      5      10

```

```

°   Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
    15      20      25
    Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Gly Pro
        30      35      40
    Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
        45      50      55
    Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
        60      65      70
5   Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
        75      80
    Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
        85      90      95
    Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Thr Asp Pro
        100      105      110
    Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
        115      120      125
10  Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
        130      135      140
    Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
        145      150
    Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
        155      160      165
    Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
        170      175      180
15  Ser Cys Leu Thr Thr Pro Ala Ser Ala
        185      190

```

(2) INFORMATION FOR SEQ ID NO: 173:

```

20      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 191 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS: unknown
          (D) TOPOLOGY: unknown

      (vi) ORIGINAL SOURCE:
          (A) ORGANISM: homosapiens
          (C) INDIVIDUAL ISOLATE: HK5

25      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1      5      10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15      20      25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Gly Pro
30      35      40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45      50      55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
60      65      70

```

35

° Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro His Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 5 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Ile Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 10 Ser Cys Leu Thr Thr Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 15
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK4
 20
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Glu Gly Arg Thr Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 30 Leu Tyr Gly Asn Glu Gly Met Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125

° Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Val Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 5 Ser Cys Leu Thr Ile Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 10
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: P8
 15
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:
 Met Ser Thr Thr Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Ser Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 20 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Pro Glu Gly Arg Ala Trp Ala Gln Pro Gly His Pro Trp Pro
 75 80
 25 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 30 Gly Gly Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Val Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180

° Ser Cys Leu Thr Ile Pro Ala Ser Ala
185 190

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:
5 (A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T3

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
15	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30					35					40			
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45					50				55			
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
			60				65						70	
	Pro	Glu	Gly	Arg	Ala	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
				75			80							
20	Leu	Tyr	Gly	Asp	Glu	Gly	Met	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Thr	Asp	Pro
	100					105					110			
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115				120					125			
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
		130				135							140	
25	Gly	Ala	Pro	Leu	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
			145			150								
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
		170				175					180			
	Ser	Cys	Leu	Thr	Ile	Pro	Ala	Ser	Ala					
30			185					190						

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 191 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: T4

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1          5          10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15          20          25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
10          30          35          40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
          45          50          55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
          60          65          70
Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
          75          80          85
Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
15          90          95          100
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
          105          110          115
Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
          120          125          130
Thr Cys Ser Leu Ala Asp Leu Met Gly Tyr Val Pro Val Val
          135          140          145
20 Gly Gly Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
          150          155          160
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
          165          170          175
Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
          180          185          190
Ser Cys Ile Thr Ile Pro Val Ser Ala
          190

```

25 (2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: US10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

35

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Pro Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ile Thr Ile Pro Val Ser Ala
 185 190

20

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T9

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

30

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Ile Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Thr Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55

35

Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80 85
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 90 95
 5 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Ser Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 10 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ile Thr Thr Pro Ala Ser Ala
 185 190

15 (2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

25 Met Ser Thr Ile Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 30 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110

35

Arg His Arg Ser Arg Asn Val Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ile Thr Ile Pro Val Ser Ala
 185 190

10 (2) INFORMATION FOR SEQ ID NO: 181:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: T8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Arg Val Ile Asp Thr Ile
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165

35

Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Phe Thr Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: US1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Ala Thr Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK11

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
10	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35						40			
	Arg	Leu	Gly	Val	Arg	Thr	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50						55			
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg
	60				65						70			
15	Ser	Thr	Gly	Lys	Pro	Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80									
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90					95				
	Ser	Pro	Arg	Gly	Ser	His	Pro	Asn	Trp	Gly	Pro	Thr	Asp	Pro
	100				105						110			
	Arg	His	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Ile
	115				120						125			
20	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Val	Val
	130				135									
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
	145				150									
	Val	Arg	Val	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
	155				160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
	170				175						180			
25	Ser	Cys	Cys	Thr	Val	Pro	Val	Ser	Ala					
	185				190									

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens

o

(C) INDIVIDUAL ISOLATE: SW3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 5 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 10 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser His Pro Asn Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
 115 120 125
 15 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 20 Ser Cys Phe Thr Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: DK8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25

° Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Ser Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Ser Thr Gly Lys Ser Trp Gly Lys Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Thr Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Ile
 115 120 125
 10 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 15 Ser Cys Cys Thr Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 186:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S83
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 30 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Asp Arg Arg
 60 65 70
 Thr Thr Gly Lys Ser Trp Gly Arg Pro Gly Tyr Pro Trp Pro
 75 80

Leu Tyr Gly Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Thr Asp Pro
 100 105 110
 Arg His Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 5 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 10 Ser Cys Ile Ser Val Pro Val Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 25 Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 30 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140

Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 5 Ser Cys Leu Ile His Pro Ala Ala Ser
 185 190

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 10
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S52
 15
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:
 Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Ile Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Val Leu Pro Arg Arg Gly Pro
 30 35 40
 20 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 25 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 30 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Phe Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 Ser Cys Leu Val His Pro Ala Ala Ser
 185 190
 35

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: S2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
1				5					10				
Thr	Ile	Arg	Arg	Pro	Gln	Asp	Ile	Lys	Phe	Pro	Gly	Gly	Gly
15				20					25				
Gln	Ile	Val	Gly	Gly	Val	Tyr	Val	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40			
Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45						50				55		
Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
		60					65				70		
Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
			75				80						
Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
85				90					95				
Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
	100				105					110			
Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	115				120						125		
Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	130				135							140	
Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
	145						150						
Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn
155				160					165				
Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe
	170				175					180			
Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser					
	185					190							

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown

o

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: DK12

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

	Met	Ser	Thr	Leu	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Ile	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20					25			
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Val	Leu	Pro	Arg	Arg	Gly	Pro
		30				35					40			
10	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
		45						50				55		
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
		60						65					70	
	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
					75					80				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
		85				90					95			
15	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
		100					105					110		
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
		115					120					125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
			130					135					140	
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
				145					150					
20	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Phe	Ala	Thr	Gly	Asn
		155			160					165				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Phe
		170				175						180		
	Ser	Cys	Leu	Ile	His	Pro	Ala	Ala	Ser					
			185					190						

25

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

30

(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

(A) ORGANISM: homosapiens

(C) INDIVIDUAL ISOLATE: Z4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

35

5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55
 60
 65
 70
 75
 80
 85
 90
 95
 100
 105
 110
 115
 120
 125
 130
 135
 140
 145
 150
 155
 160
 165
 170
 175
 180
 185
 190

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 Pro Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Ile Val
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 Ser Cys Leu Thr Val Pro Ala Ser Ala

(2) INFORMATION FOR SEQ ID NO: 192:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z8

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser

° Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 70
 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 5 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 10 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 193:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z1

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 25 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Ala Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 30 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110

35

° Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 5 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 194:

10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 20 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Gln Ala Arg Arg
 60 65 70
 25 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Gln Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 30 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165

35

° Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Phe
 170 175 180
 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 195:

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 10 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: Z6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
 15 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Arg
 60 65 70
 20 Ser Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 25 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Val Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 30 Ser Cys Leu Thr Val Pro Thr Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 196:

35 (i) SEQUENCE CHARACTERISTICS:

o

(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

5 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: Z7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
10	Thr	Asn	Arg	Arg	Pro	Met	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Thr	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Arg
	60				65					70				
15	Ser	Glu	Gly	Arg	Ser	Trp	Ala	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Gly	Asn	Glu	Gly	Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	90				95					100				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
	105				110					115				
	Arg	Arg	Arg	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	120				125					130				
20	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	135				140					145				
	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
	150				155					160				
	Val	Arg	Ala	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala	Thr	Gly	Asn
	165				170					175				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Leu	Leu	Ala	Leu	Leu
25	180				185					190				
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:

35 (A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: DK13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1      5      10
Thr Asn Arg Arg Pro Met Asp Val Lys Phe Pro Gly Gly Gly
15      20      25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30      35      40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45      50      55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
60      65      70
Leu Glu Gly Arg Ser Trp Ala Gln Pro Gly Tyr Pro Trp Pro
75      80
Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
85      90      95
Ser Pro Arg Gly Ser Arg Pro Ser Trp Gly Pro Asn Asp Pro
100      105      110
Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115      120      125
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
130      135      140
Gly Ala Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
145      150
Val Arg Leu Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155      160      165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
170      175      180
Ser Cys Leu Thr Val Pro Ala Ser Ala
185      190

```

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

```

(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

```

(vi) ORIGINAL SOURCE:

```

(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SA4

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

```

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1      5      10
Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15      20      25

```

° Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 5 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 10 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 15 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 20
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA5
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:
 25 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 30 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 35

Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

10

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

20

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150

35

o

Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155 160 165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
170 175 180
Ser Cys Leu Thr Val Pro Ala Ser Ala
185 190

5

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 191 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

10

(vi) ORIGINAL SOURCE:
(A) ORGANISM: homosapiens
(C) INDIVIDUAL ISOLATE: SAI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

15

Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
1 5 10
Thr Asn Leu Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
15 20 25
Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
30 35 40
Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
45 50 55
Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
60 65 70
Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
75 80
Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
85 90 95
Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
100 105 110
Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
115 120 125
Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
130 135 140
Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
145 150
Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
155 160 165
Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
170 175 180
Ser Cys Leu Ile Ile Pro Ala Ser Ala
185 190

35

o

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

10	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15				20					25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
	30				35					40				
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
	45				50					55				
15	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Gln
	60				65					70				
	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
	75				80					85				
	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Glu	Trp	Ala	Gly	Trp	Leu	Leu
	90				95					100				
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Ser	Trp	Gly	Pro	Asn	Asp	Pro
	105				110					115				
20	Arg	Arg	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
	120				125					130				
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
	135				140					145				
	Gly	Gly	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
	150				155					160				
25	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
	165				170					175				
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu
	180				185					190				
	Ser	Cys	Leu	Thr	Val	Pro	Ala	Ser	Ala					

30

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

35

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA13

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

5	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn
	1				5					10				
	Thr	Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly
	15					20				25				
	Gln	Ile	Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro
		30					35					40		
	Arg	Leu	Gly	Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser
			45					50					55	
10	Gln	Pro	Arg	Gly	Arg	Arg	Gln	Pro	Ile	Pro	Lys	Ala	Arg	Gln
			60					65					70	
	Pro	Thr	Gly	Arg	Ser	Trp	Gly	Gln	Pro	Gly	Tyr	Pro	Trp	Pro
				75					80					
	Leu	Tyr	Ala	Asn	Glu	Gly	Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu
	85				90				95					
	Ser	Pro	Arg	Gly	Ser	Arg	Pro	Asn	Trp	Gly	Pro	Asn	Asp	Pro
	100					105					110			
15	Arg	Arg	Lys	Ser	Arg	Asn	Leu	Gly	Lys	Val	Ile	Asp	Thr	Leu
			115					120				125		
	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly	Tyr	Ile	Pro	Leu	Val
			130					135					140	
	Gly	Gly	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala	Leu	Ala	His	Gly
				145				150						
	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Tyr	Ala	Thr	Gly	Asn
20	155				160				165					
	Leu	Pro	Gly	Cys	Ser	Phe	Ser	Ile	Phe	Ile	Leu	Ala	Leu	Leu
		170				175					180			
	Ser	Cys	Leu	Thr	Val	Pro	Thr	Ser	Ala					
			185				190							

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

35	Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Gln	Arg	Asn
	1				5					10				

5 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 Arg Met Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 Ser Ala Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 Leu Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 Arg Arg Lys Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 Val Arg Val Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 Leu Pro Gly Cys Ser Phe Ser Ile Phe Val Leu Ala Leu Leu
 170 Ser Cys Leu Thr Val Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 205:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

 25 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: SA11

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:
 Met Ser Thr Asn Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 30 Thr Asn Arg Arg Pro Gln Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70

°

Pro Thr Gly Arg Ser Trp Gly Gln Pro Gly Tyr Pro Trp Pro
 75 80
 Phe Tyr Ala Asn Glu Gly Leu Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro Asn Trp Gly Pro Asn Asp Pro
 100 105 110
 5 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125
 Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Leu Val
 130 135 140
 Gly Gly Pro Val Gly Gly Val Ala Arg Ala Leu Ala His Gly
 145 150
 Val Arg Ala Leu Glu Asp Gly Val Asn Tyr Ala Thr Gly Asn
 155 160 165
 10 Leu Pro Gly Cys Ser Phe Ser Ile Phe Ile Leu Ala Leu Leu
 170 175 180
 Ser Cys Leu Thr Val Pro Ala Thr Ala
 185 190

(2) INFORMATION FOR SEQ ID NO: 206:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: homosapiens
 (C) INDIVIDUAL ISOLATE: HK2
- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

Met Ser Thr Leu Pro Lys Pro Gln Arg Lys Thr Lys Arg Asn
 1 5 10
 Thr Asn Arg Arg Pro Thr Asp Val Lys Phe Pro Gly Gly Gly
 15 20 25
 25 Gln Ile Val Gly Gly Val Tyr Leu Leu Pro Arg Arg Gly Pro
 30 35 40
 Arg Leu Gly Val Arg Ala Thr Arg Lys Thr Ser Glu Arg Ser
 45 50 55
 Gln Pro Arg Gly Arg Arg Gln Pro Ile Pro Lys Ala Arg Gln
 60 65 70
 Pro Gln Gly Arg His Trp Ala Gln Pro Gly Tyr Pro Trp Pro
 75 80
 30 Leu Tyr Gly Asn Glu Gly Cys Gly Trp Ala Gly Trp Leu Leu
 85 90 95
 Ser Pro Arg Gly Ser Arg Pro His Trp Gly Pro Asn Asp Pro
 100 105 110
 Arg Arg Arg Ser Arg Asn Leu Gly Lys Val Ile Asp Thr Leu
 115 120 125

° Thr Cys Gly Phe Ala Asp Leu Met Gly Tyr Ile Pro Val Val
 130 135 140
 Gly Ala Pro Leu Gly Gly Val Ala Ala Leu Ala His Gly
 145 150
 Val Arg Ala Ile Glu Asp Gly Ile Asn Tyr Ala Thr Gly Asn
 155 160 165
 Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala Leu Leu
 170 175 180
 5 Ser Cys Leu Thr Thr Pro Ala Ser Ala
 185 190

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

15 GCGTCCGGGT TCTGGAAGAC GCGGTGAAC TATCAACAGG 40

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGCTTTCAT TGCAGTTCAA GGCCGTGCTA TTGATGTGCC 40

25 (2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

AAGACGGCGT GAACTATGCA ACAGGGAACC TTCCTGGTTG 40

(2) INFORMATION FOR SEQ ID NO:210:

35

- 0
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:
 AGTTCAAGGC CGTGCTATTG ATGTGCCAAC TGCCGTTGGT 40
- (2) INFORMATION FOR SEQ ID NO:211:
- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:
 15 AAGACGGCGT GAATTCTGCA ACAGGGAACC TTCCTGGTTG 40
- (2) INFORMATION FOR SEQ ID NO:212:
- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:
 AGTTCAAGGC CGTGGAATTC ATGTGCCAAC TGCCGTTGGT 40
- 25 (2) INFORMATION FOR SEQ ID NO:213:
- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:
 ARCTYCGACG TYACATCGAY CTGCTYGTYG GRAGYGCCAC CC 42
- (2) INFORMATION FOR SEQ ID NO:214:

- °
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:
RCARGCCRTC TTGGAYATGA TCGCTGGWGC Y 31
- (2) INFORMATION FOR SEQ ID NO:215:
- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
15 CRATACGACR YCAYGTCGAY TTGCTCGTTG GGGCGGCTRY YT 42
- (2) INFORMATION FOR SEQ ID NO:216:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:
RCAAGCTRTC RTGGAYRTGG TRRCRGGRGC C 31
- 25 (2) INFORMATION FOR SEQ ID NO:217:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:
TTGCGGACKC ACATYGACAT GGTYGTGATG TCCGCCACGC 40
- (2) INFORMATION FOR SEQ ID NO:218:

°

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:
 GATGCGCGTT CCCGAGGTCA TCWTAGACAT CRTYRGCGGR GCD 43

(2) INFORMATION FOR SEQ ID NO:219:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:
 15 AATGGCACCY TGCRCCTGCTG GATACAAGTR ACACCTAATG TGGCTGTGAA 50
 ACAC 54

(2) INFORMATION FOR SEQ ID NO:220:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:
 TGARCTAGYC CTYSARGTYG TCTTCGGYGG Y 31

25 (2) INFORMATION FOR SEQ ID NO:221:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:
 GCCAACGTCT CTCGATGTTG GGTGCCGTT GCCCCCAATC TCGCCATAAG 50
 TCAA 54

o

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AAGGGCCTGC GAGCACACAT CGATATCATC GTGATGTCTG CTACGG 46

(2) INFORMATION FOR SEQ ID NO:223:

10

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

TTGGTGC GCA TCCCGAAGT CATCTTGAT ATTGTTACAG GAGGT 45

(2) INFORMATION FOR SEQ ID NO:224:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

AGTCAGGTAY GTCGGAGCAA CCACCGCYTC GATACGCAGT 40

(2) INFORMATION FOR SEQ ID NO:225:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

AGCCTTCACG TTCAGACCKC GTCGCCATCA AACRGTCAG ACCTGT 46

35

- °
- (2) INFORMATION FOR SEQ ID NO:226:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:
- TCCCCCGCYG TGGGTATGGT GGTRGCGCAC RTYCTGCGDY TGCCCCAGAC 50
CKTGTTYGAC ATAMTRGCGY GGGCC 75
- 10 (2) INFORMATION FOR SEQ ID NO:227:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:
- ACGCCGGTGA CGCCTACAGT GGCTGTCGCA CACCCGGGC 39
- (2) INFORMATION FOR SEQ ID NO:228:
- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:
- 25 ATGAGGGTCC CCACAGCCTT TCTCGACATG GTTGCCGGAG GC 42
- (2) INFORMATION FOR SEQ ID NO:229:
- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:
- CGCGCCCTAT CCCAACGCAC CGTTAGAGTC CATGCGCAGG 40

o

(2) INFORMATION FOR SEQ ID NO:230:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

TCAGATCTTA CGGATCCCCT CTATCCTAGG TGACTTGCTC ACCGGGGGT 49

10 (2) INFORMATION FOR SEQ ID NO:231:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

CAGTCACGCT GCTGGGTGGC CCTTACTCCC ACCGTGGCGG YGYCTTATAT 50
 CGGT 54

(2) INFORMATION FOR SEQ ID NO:232:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

25 TAGCACTCTG GTRGAYCTAC TCRCTGGAGG G 31

(2) INFORMATION FOR SEQ ID NO:233:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

35 AAGTCTACAT GCTGGGTGTC TCTACCCCC ACCGTGGCTG CGAACATCT 50

GAAT 54

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:
 AGGCGCCATG GTCGACCTGC TTGCAGGCGG C 31

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:
 TCAGCCCCGA VYYTCGGAGC GGTACAGGCT CCTCTTCGGA GGG 43

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:
 TGYTACGGAT YCCCCARGTG GTCATHGACA TCATWGCCGG GGSC 44

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:
 CATACCAAAT GCTTCCACGC CCGCAACGGG ATTCGCGAGG 40

o

(2) INFORMATION FOR SEQ ID NO:238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

TCTTCTTGCG GCGCCGCGAG TGGTTTGCTC ATCCCTG 37

10 (2) INFORMATION FOR SEQ ID NO:239:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

ATCTAGCATC TTGAGGGTAC CTGAGATTG TGCGAGTGTG ATATTGGTG 50
 GC 52

(2) INFORMATION FOR SEQ ID NO:240:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

Trp	Ile	Gln	Val	Thr	Pro	Asn	Val	Ala	Val	Lys	His	Arg	Gly	Ala	
						5			10					15	
Leu	Thr	His	Asn	Leu	Arg	Xaa	His	Xaa	Asp	Xaa	Ile	Val	Met	Ala	
					20				25					30	
Ala	Thr	Val													

30 (2) INFORMATION FOR SEQ ID NO:241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

35

o

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Trp Val Pro Val Ala Pro Asn Leu Ala Ile Ser Gln Pro Gly Ala
 5 10 15
 Leu Thr Lys Gly Leu Arg Ala His Ile Asp Ile Ile Val Met Ser
 20 25 30
 5 Ala Thr Val

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Trp Ile Pro Val Xaa Pro Asn Val Ala Val Xaa Xaa Pro Gly Ala
 5 10 15
 Leu Thr Gln Gly Leu Arg Thr His Ile Asp Met Val Val Met Ser
 20 25 30
 15 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Trp Thr Xaa Val Thr Pro Thr Val Ala Val Arg Tyr Val Gly Ala
 5 10 15
 Thr Thr Ala Ser Ile Arg Ser His Val Asp Leu Leu Val Gly Ala
 20 25 30
 25 Ala Thr Xaa

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown
 35

o

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Trp Val Ala Leu Xaa Pro Thr Leu Ala Ala Arg Asn Xaa Xaa Xaa
 Xaa Thr Xaa Xaa Ile Arg Xaa His Val Asp Leu Leu Val Gly Ala
 Ala Xaa Phe

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

Trp Val Xaa Xaa Xaa Pro Thr Val Ala Thr Arg Asp Gly Lys Leu
 Pro Xaa Xaa Gln Leu Arg Arg Xaa Ile Asp Leu Leu Val Gly Ser
 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

Trp Thr Pro Val Thr Pro Thr Val Ala Val Ala His Pro Gly Ala
 Pro Leu Glu Ser Phe Arg Arg His Val Asp Leu Met Val Gly Ala
 Ala Thr Leu

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

o

Trp	Val	Ala	Leu	Thr	Pro	Thr	Val	Ala	Xaa	Xaa	Tyr	Ile	Gly	Ala	
				5					10					15	
Pro	Leu	Xaa	Ser	Xaa	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	
				20					25					30	
Ala	Thr	Val													

5

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Trp	Val	Ser	Leu	Thr	Pro	Thr	Val	Ala	Ala	Gln	His	Leu	Asn	Ala	
				5					10					15	
Pro	Leu	Glu	Ser	Leu	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Gly	
				20					25					30	
Ala	Thr	Leu													

15

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Trp	Val	Pro	Leu	Thr	Pro	Thr	Val	Ala	Ala	Pro	Tyr	Pro	Asn	Ala	
				5					10					15	
Pro	Leu	Glu	Ser	Met	Arg	Arg	His	Val	Asp	Leu	Met	Val	Gly	Ala	
				20					25					30	
Ala	Thr	Met													

25

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

35

° Trp Val Xaa Ile Thr Pro Thr Leu Ser Ala Pro Xaa Xaa Gly Ala
 5 10 15
 Val Thr Ala Pro Leu Arg Arg Xaa Val Asp Tyr Leu Ala Gly Gly
 20 25 30
 Ala Ala Leu

(2) INFORMATION FOR SEQ ID NO:251:

5

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

10

Trp His Ala Val Thr Pro Thr Leu Ala Ile Pro Asn Ala Ser Thr
 5 10 15
 Pro Ala Thr Gly Phe Arg Arg His Val Asp Leu Leu Ala Gly Ala
 20 25 30
 Ala Val Val

15

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Thr Leu Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro Glu Leu
 5 10 15
 Xaa Leu Xaa Val Val Phe Gly Gly
 20

25

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Thr Thr Thr Met Leu Leu Ala Tyr Leu Val Arg Ile Pro Glu Val
 5 10 15
 Ile Leu Asp Ile Val Thr Gly Gly
 20

35

o

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Thr Xaa Thr Xaa Ile Leu Ala Tyr Xaa Met Arg Val Pro Glu Val
 5 10 15
 Ile Xaa Asp Ile Xaa Xaa Gly Ala
 20

10

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Ala Val Gly Met Val Val Ala His Xaa Leu Arg Leu Pro Gln Thr
 5 10 15
 Xaa Phe Asp Ile Xaa Ala Gly Ala
 20

20

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

Thr Xaa Ala Leu Val Xaa Ser Gln Leu Leu Arg Xaa Pro Gln Ala
 5 10 15
 Xaa Xaa Asp Xaa Val Xaa Gly Ala
 20

30

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids

35

o

(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

5 Thr Xaa Ala Leu Val Xaa Ala Gln Leu Leu Arg Xaa Pro Gln Ala
5 10 15
Xaa Leu Asp Met Ile Ala Gly Ala
20

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

15 Thr Thr Thr Leu Leu Leu Ala Gln Ile Met Arg Val Pro Thr Ala
5 10 15
Phe Leu Asp Met Val Ala Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:259:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

25 Thr Thr Thr Leu Xaa Leu Ala Gln Val Met Arg Ile Pro Ser Thr
5 10 15
Leu Val Asp Leu Leu Xaa Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:260:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

35

Thr Ala Thr Leu Val Leu Ala Gln Leu Met Arg Ile Pro Gly Ala
5 10 15
Met Val Asp Leu Leu Ala Gly Gly
20

5 (2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Thr Ser Ala Leu Ile Met Ala Gln Ile Leu Arg Ile Pro Ser Ile
5 10 15
Leu Gly Asp Leu Leu Thr Gly Gly
20

15 (2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Xaa Thr Ala Leu Xaa Met Ala Gln Xaa Leu Arg Ile Pro Gln Val
5 10 15
Val Ile Asp Ile Ile Ala Gly Xaa
20

25 (2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

Thr Thr Thr Leu Val Leu Ser Ser Ile Leu Arg Val Pro Glu Ile
5 10 15
Cys Ala Ser Val Ile Phe Gly Gly
20

35

CLAIMS

1. A purified and isolated DNA having a sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51.

2. A purified and isolated protein encoded by a gene whose sequence includes a sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102.

3. A purified and isolated DNA having a sequence selected from the group consisting of SEQ ID NO: 103 through SEQ ID NO: 154.

4. A purified and isolated protein encoded by a gene sequence selected from the group consisting of SEQ ID NO: 155 through SEQ ID NO: 206.

5. A purified and isolated protein having an amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102 and SEQ ID NO:155 through SEQ ID NO:206.

6. A method for the recombinant DNA-directed synthesis of a protein, said method comprising:
culturing a transformed or transfected host organism containing a DNA sequence capable of directing the host organism to produce said protein under conditions such that the protein is produced, said protein exhibiting substantial homology to a protein comprising the amino acid sequence selected from the group consisting of SEQ ID NO:52 through SEQ ID NO:102 or SEQ ID NO:155 through SEQ ID NO:206.

° 7. The method of claim 6, wherein the host organism is transfected with a recombinant eukaryotic expression vector.

8. The method of claim 7, wherein the host
5 organism is a eukaryotic cell.

9. A recombinant expression vector comprising a DNA sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:51 and SEQ ID NO:103 through SEQ ID
10 NO:154.

10. A host organism transformed or transfected with a recombinant expression vector according to claim 9.

15 11. A method of detecting antibodies against HCV, said method comprising:

- (a) contacting a biological sample with at least one protein of claim 5 to form an immune complex with the antibodies; and
- 20 (b) detecting the presence of the immune complex.

12. The method of claim 11 wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.
25

13. The method of claim 11, wherein the recombinant protein is bound to a solid support.

30 14. The method of claim 11, wherein the immune complex is detected using a labeled antibody.

15. A hepatitis C virus kit comprising: at least one protein comprising an amino acid sequence selected from the group consisting of: SEQ ID NO:52 through SEQ ID NO:102
35

° and SEQ ID NO:155 through SEQ ID NO:206.

16. A composition comprising at least one recombinant protein of claim 5 and an excipient, diluent or carrier.

5 17. A composition comprising an expression vector capable of directing host organism synthesis of a protein having an amino acid sequence selected from the group consisting of SEQ ID NO: 52 through SEQ ID NO: 102 and SEQ ID NO: 155 through SEQ ID NO: 206.

10 18. A method of preventing hepatitis C infection, comprising administering the composition of claim 16 or 17 to a mammal in an effective amount to stimulate the production of protective antibody.

15 19. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one protein according to claim 5 in a pharmacologically acceptable carrier.

20 20. A vaccine for immunizing a mammal against hepatitis C infection, said vaccine comprising an expression vector capable of directing host organism synthesis of a protein having an amino acid sequence
25 selected from the group consisting of SEQ ID NO:52 - SEQ ID NO:102 and SEQ ID NO:155 - SEQ ID NO:206.

30 21. A method for detecting the presence of the hepatitis C virus via a reverse transcription-polymerase chain reaction, said method comprising amplifying an HCV reverse transcription product by polymerase chain reaction using universal primers.

35 22. The method of claim 21, wherein said universal primers are deduced from universally conserved

- ° nucleotide domains found in SEQ ID NO: 1 through SEQ ID NO: 51, in SEQ ID NO: 103 through SEQ ID NO: 154, or in consensus sequences shown in Figures 1A-H and 6A-K.

23. Substantially isolated and purified
5 universal primers, wherein said primers have nucleic acid sequences derived from universally conserved nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID NO:154 and in consensus sequences showing Figures 1A-H and 6A-K.

10

24. A diagnostic kit for use in detecting the presence of hepatitis C virus in a biological sample, said kit comprising at least two universal primers according to claim 22.

15

25. A diagnostic kit for use in detecting the presence of hepatitis C virus in a biological sample, said kit comprising at least one nucleic acid sequence selected from the group consisting of SEQ ID No:1-51 or SEQ ID No:103-154.

20

26. A method for determining the genotype of a hepatitis C virus, said method comprising:
amplifying reverse transcription
25 products of RNA via polymerase chain reaction using genotype-specific amplification primers deduced from genotype-specific nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID NO:154, or in consensus sequences shown in Figures 1A-H and 6A-K.

30

27. A method for determining the genotype of a hepatitis C virus, said method comprising:

35

- °
- (a) amplifying RNA via reverse transcription-polymerase chain reaction to produce amplification products;
 - (b) contacting said products with at least one sequence shown in SEQ ID NO:1 through SEQ ID NO:51 and SEQ ID NO:103 through SEQ ID NO:154; and
 - (c) detecting complexes of said product which bind to said nucleic acid sequence.
- 5
- 10

28. A method for determining the genotype of a hepatitis C virus, said method comprising:

- (a) amplifying RNA via reverse transcription-polymerase chain reaction to produce amplification products;
 - (b) contacting said products with at least one genotype-specific oligonucleotide; and
 - (c) detecting complexes of said products which bind to said oligonucleotide(s).
- 15
- 20

29. The method of claims 27 or 28, wherein said amplification of step (a) uses universal primers deduced from universally conserved nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID NO:154, or in consensus sequences shown in Figures 1A-H and 6A-K.

25

30. The method of claim 28, wherein said genotype-specific oligonucleotide of step (b) is a nucleic acid sequence deduced from genotype-specific nucleotide domains found in SEQ ID NO:1 through SEQ ID NO:51 and SEQ ID NO:103 through SEQ ID NO:154, or in consensus sequences shown in Figures 1A-H and 6A-K.

30

35

° 31. Substantially isolated and purified
genotype-specific oligonucleotides, wherein said
oligonucleotides have nucleic acid sequences deduced from
genotype-specific nucleotide domains found in SEQ ID NO:1
through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID
5 NO:154, or in consensus sequences shown in Figures 1A-H and
6A-K.

 32. Substantially purified and isolated
genotype-specific peptides having amino acid sequences
10 deduced from a genotype-specific amino acid domains located
in SEQ ID NO:52 through SEQ ID NO:102, in SEQ ID NO:155
through SEQ ID NO:206, or in consensus sequences shown in
Figures 2A-H and 7A-K.

15 33. A method of detecting antibodies specific
for a single genotype of HCV, said method comprising:
 (a) contacting a biological sample with at
 least one peptide of claim 32 to form
 an immune complex with the antibodies,
20 and
 (b) detecting the presence of the immune
 complex.

 34. The method of claim 33, wherein the
25 biological sample is selected from the group consisting of
serum, saliva or lymphocytes or other mononuclear cells.

 35. The method of claim 33, wherein said peptide
is bound to a solid support.

30 36. The method of claim 33, wherein the immune
complex is detected using a labelled antibody or antigen.

 37. A kit for use in detecting antibodies
35 specific for a single genotype of HCV, said kit comprising:

- ° at least one peptide selected from the genotype-specific peptides of claim 32.

38. Substantially purified and isolated universal peptides having amino acid sequences deduced from
5 universally conserved amino acid domains found in SEQ ID NO:52 through SEQ ID NO:102, in SEQ ID NO:155 through SEQ ID NO:206, or in consensus sequences shown in Figures 2A-H and 7A-K.

10 39. A method of detecting antibodies against all genotypes of HCV, said method comprising:

- (a) contacting a biological sample with at least one peptide of claim 38 to form an immune complex with the antibodies,
15 and
- (b) detecting the presence of the immune complex.

20 40. The method of claim 39, wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.

41. The method of claim 39, wherein said peptide is bound to a solid support.

25 42. The method of claim 39, wherein the immune complex is detected using a labelled antibody or antigen.

30 43. A composition comprising at least one peptide of claim 32 and an excipient, diluent or carrier.

44. A composition comprising at least one peptide of claim 38 and an excipient, diluent or carrier.

35 45. A method of preventing hepatitis C

° 31. Substantially isolated and purified
genotype-specific oligonucleotides, wherein said
oligonucleotides have nucleic acid sequences deduced from
genotype-specific nucleotide domains found in SEQ ID NO:1
through SEQ ID NO:51, in SEQ ID NO:103 through SEQ ID
5 NO:154, or in consensus sequences shown in Figures 1A-H and
6A-K.

 32. Substantially purified and isolated
genotype-specific peptides having amino acid sequences
10 deduced from a genotype-specific amino acid domains located
in SEQ ID NO:52 through SEQ ID NO:102, in SEQ ID NO:155
through SEQ ID NO:206, or in consensus sequences shown in
Figures 2A-H and 7A-K.

15 33. A method of detecting antibodies specific
for a single genotype of HCV, said method comprising:
 (a) contacting a biological sample with at
 least one peptide of claim 32 to form
 an immune complex with the antibodies,
20 and
 (b) detecting the presence of the immune
 complex.

 34. The method of claim 33, wherein the
25 biological sample is selected from the group consisting of
serum, saliva or lymphocytes or other mononuclear cells.

 35. The method of claim 33, wherein said peptide
is bound to a solid support.

30 36. The method of claim 33, wherein the immune
complex is detected using a labelled antibody or antigen.

 37. A kit for use in detecting antibodies
35 specific for a single genotype of HCV, said kit comprising:

- ° at least one peptide selected from the genotype-specific peptides of claim 32.

38. Substantially purified and isolated universal peptides having amino acid sequences deduced from
5 universally conserved amino acid domains found in SEQ ID NO:52 through SEQ ID NO:102, in SEQ ID NO:155 through SEQ ID NO:206, or in consensus sequences shown in Figures 2A-H and 7A-K.

10 39. A method of detecting antibodies against all genotypes of HCV, said method comprising:

- (a) contacting a biological sample with at least one peptide of claim 38 to form an immune complex with the antibodies,
15 and
(b) detecting the presence of the immune complex.

20 40. The method of claim 39, wherein the biological sample is selected from the group consisting of serum, saliva or lymphocytes or other mononuclear cells.

41. The method of claim 39, wherein said peptide is bound to a solid support.

25 42. The method of claim 39, wherein the immune complex is detected using a labelled antibody or antigen.

30 43. A composition comprising at least one peptide of claim 32 and an excipient, diluent or carrier.

44. A composition comprising at least one peptide of claim 38 and an excipient, diluent or carrier.

35 45. A method of preventing hepatitis C

- ° infection, comprising administering the composition of claims 43 or 44 to a mammal in an effective amount to stimulate production of a protective antibody.

46. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one peptide according to claims 32 or 38 in a pharmaceutically acceptable carrier.

47. A composition comprising at least one expression vector capable of directing host organism synthesis of a genotype-specific peptide having amino acid sequence deduced from a genotype-specific amino acid domain located in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID NO:155 - SEQ ID NO:206, or in consensus sequences shown in figures 2A-H and 7A-K.

48. A composition comprising at least one expression vector capable of directing host organism synthesis of a universal peptide having amino acid sequence deduced from universally conserved amino acid domains found in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID NO:155 - SEQ ID NO:206, or in consensus sequences shown in figures 2A-H and 7A-K.

49. A method of preventing hepatitis C infection, comprising administering the composition of claims 47 or 48 to a mammal in an effective amount to stimulate production of a protective antibody.

50. A vaccine for immunizing a mammal against hepatitis C infection, said vaccine comprising at least one expression vector capable of directing host organism synthesis of a geno-type specific peptide having amino acid sequence deduced from a geno type-specific amino acid domain located in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID

- ° NO:155 - SEQ ID NO:206, or in consensus sequences shown in figures 2A-H and 7A-K.

51. A vaccine for immunizing a mammal against hepatitis C infection, comprising at least one expression
5 vector capable of directing host organism synthesis of a universal peptide having amino acid sequence deduced from universally conserved amino acid domain found in SEQ ID NO:52 - SEQ ID NO:102, and SEQ ID NO:155 - SEQ ID NO:206, or in consensus sequences shown in figures 2A-H and 7A-K.

10

52. Anti-HCV core antibodies having specific binding affinity for core protein of a single genotype of HCV.

15

53. Anti-HCV envelope 1 antibodies having specific binding affinity for envelope 1 protein of a single genotype of HCV.

20

54. The antibodies of claims 52 or 53 wherein said antibodies are monoclonal antibodies.

55. A method of detecting core protein specific for a single genotype of HCV, said method comprising:

- 25 (a) contacting a biological sample with at least one antibody of claim 52 to form an immune complex with said core protein, and
(b) detecting the presence of the immune complex.

30

56. A method of detecting E1 protein specific for a single genotype of HCV, said method comprising:

- 35 (a) contacting a biological sample with at least one antibody of claim 53 to form an immune complex with said E1 protein;

o

and

- (b) detecting the presence of the immune complex.

57. The methods of claims 55 or 56, wherein the
5 biological sample is selected from the group consisting of serum, saliva lymphocytes or other mononuclear cells and liver.

58. The method of claims 55 or 56, wherein said
10 antibody is bound to a solid support.

59. A method of detecting antibodies against all
genotypes of HCV, said method comprising:

- (a) contacting a biological sample with at
15 least one universal peptide of claim 38 to form an immune complex with said antibodies; and
- (b) detecting the presence of the immune complex.

20

25

30

35

o

ABSTRACT

The nucleotide and deduced amino acid sequences of cDNAs encoding the envelope 1 genes and core genes of isolates of hepatitis C virus (HCV) are disclosed. The invention relates to the oligonucleotides, peptides and recombinant envelope 1 and core proteins derived from these sequences and their use in diagnostic methods and vaccines.

10

15

20

25

30

35

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTACCAATGATTGCCCTAACTCGAGTA
1	DK7	1 TACCAAGTGC GCAACTCCACGGGGCTTTACCATGTACCAATGATTGCCCTAACTCGAGTA
9	US11	1 TACCAAGTAC GCAACTCCACGGGGCTTTACCATGTACCAATGATTGCCCTAACTCGAGTA
4	DR4	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTACCAATGATTGCCCTAACTCGAGTA
3	DR1	1 CACCAAGTGC GCAACTCTACAGGGCTTTACCATGTACCAATGATTGCCCTAACTCGAGTA
2	DK9	1 TACCAAGTAC GCAACTCCTCGGGCTTTACCATGTACCAATGATTGCCCTAACTCGAGTA
6	S18	1 TACCAAGTAC GCAACTCCACGGGGCTTTACCATGTACCAATGATGCCCTAACTCGAGCA
7	SW1	1 TACCAAGTAC GCAACTCCTCGGGCTTTACCATGTACCAATGATGCCCTAACTCGAGTA
1-8	consensus	tACCAAGT-CGCAACTCcaCgGGyCTtTACCATGTcACCAATGAtTGCCCTAAcTCGAGtA

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	62 TtGTGTACGAGaCaGctGATGCTATCCTaCacGCTCCGGGaTGTGTCCCTTGCgTTcGtGA
1	DK7	62 TcGTGTACGAGGCGGCGATGCCATCTCTGCACACTCCGGGGTGTGTCCCTTGCgTTcGCGA
8	US11	62 TTGTGTACGAGGCGGCGATGCCATCTCTGCACACTCCGGGGTGTGTCTTGCgTTcGCGA
4	DR4	62 TTGTGTACGAGGCGGCGATGCCATCTCTGCACAGCGGGGTGTGTCCCTTGCgTTcGCGA
3	DR1	62 TTGTGTACGAGGCGGCGATGCCATCTCTGCACgCGCCGGGTGTGTCCCTTGCgTTcGCGA
2	DK9	62 TTGTGTACGAGGCGGCGATGCCATCTCTGCaTCTCCaGGGTGTGTCCCTTGCgTTcGCGA
6	S18	62 TTGTGTACGAGAGCGGCGGATaCCATCTACACTCTCCgGGTGTGTCCCTTGCgTTcGCGA
7	SW1	62 TTGTGTACGAGAGCGGCGATgCCAtTCTACACTCTCCaGGGTGTGTCCCTTGCgTTcGCGA
1-8	consensus	TtGTGTACGAGGcGgCcGATgCcAtCTgCaC-CtCCgGGgTGTGTcCCTTGCgTTcGcGa

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	123 GGGTAACaCCTCGAGGTGTGGGTGGCGATGACCCCCACGGTGGCCACcAGGGaCgGCAAA
1	DK7	123 GGGTAACGCTCTCGAGGTGTGGGTGGCGATGACCCCCACGGTGGCCACcAGGGATgGCAAA
8	US11	123 GGGTAACGCTCTCGAGGTGTGGGTGGCGATGACCCCCACGGTGGCCACcAGGGACgGCAAA
4	DR4	123 GGGTAACaCCTCGAGGTGTGGGTGGCGGTGACCCCCACGGTGGCCACcAGGGACgGCAAA
3	DR1	123 GGGTAACGCCTCTCGAGGTGTGGGTGGCGGTGACCCCCACGGTGGCCACcAGGGACgGCAAF
2	DK9	123 GGGTAACGCCTCGAaATGTGGGTGGCGGTGGCCCCCAGGTGGCCACcAGGGACgGCAAg
6	S18	123 GGGTAACGCCTCGAgATGTGGGTGcCGGTGGCCCCCACAgtTgCCACcAGGGACgGCAAA
7	SW1	23 GGATggCGCCcCGAagTGTGGGTGgCGGTGGCCCCCACAgtgGCCAcTAgGGACgGCAAA
1-8	consensus	GGgTaaCgcctCGAggTGTGGGTGgCGGTGaCCCCCAGgGTgGCCAcCAGGGaCgGCAaa

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	184 CTCCCCgCAaCGCAGCTTCGACGTcACATCGATCTGCTtGTcGGGAGcGCCACCCTCTGTT
1	DK7	184 CTCCCCACAgCGCAGCTTCGACGTcACATCGATCTGCTcGTcGGGAGtGCCACCCTCTGTT
8	US11	184 CTCCCCACAACGCAaCTTCGACGTcACATCGATCTGCTtGTcGGGAGcGCCACCCTCTGTT
4	DR4	184 CTCCCCACAACGCAgCTcCGACGTcACATCGACCTGCTtGTcGGGAGcGCCACCCTCTGCT
3	DR1	184 CTCCCCACAACGCAgCTTCGACGTcACATCGACCTGCTtGTcGGGAGcGCCACCCTCTGCT
2	DK9	184 CTCCCCGCAACGCAgCTTCGACGTcACATCGATCTGCTtGTcGGGAGcGCCACCCTCTGCT
6	S18	184 CTCCCCGCAACGCAgCTTCGACGTcACATCGATCTGCTtGTtGGGAGcGCCACCCTCTGCT
7	SW1	184 CTCCTcGCAACGCAgCTTCGACGTcACATCGATCTGCTtGTcGGaAGcGCCACCCTCTGCT
1-8	consensus	CTCCCC - CAaCGCAgCTcCGACGTcACATCGATCTGCTtGTcGGgAGcGCCACCCTCTGcT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTTCTTGTCGGTCAgCTGTTTACCTT
1	DK7	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTCGGTCAaCTGTTTACCTT
8	S11	245 CGGCCCTCTACGTGGGGGACCTGTGCGGGTCTGTCTTTCTTGTCGGTCAaCTGTTTACCTT
4	DR4	245 CGGCCCTCTACGTGGGGGACtTGTGCGGGTCTGTCTTCTTGTCGGTCAaCTGTTTACCTT
3	DR1	245 CGGCCCTCTACGTGGGGGACcTGTGCGGGTCTGTCTTCTTGTCGGTCAaCTGTTTACCTT
2	DK9	245 CGGCCCTCTATGTGGGGGACtTGTGCGGGTCTGTCTTCTTGTCGGGCAaCTGTTTACCTT
6	S18	245 CGGCCCTCTATGTGGGGGACcTGTGCGGGTCTGTCTTTCTTGTCAGGCAgCTGTTTACcTaT
7	SW1	245 CGGCCCTCTAcGTGGGGGACtTGTGCGGGTCTGTCTTTCTcGTcAGTcCAaCTGTTTACcGtT
1-8	consensus	CGGCCCTCTAcGTGGGGGAC - TGTGCGGGTCTGTCTTTCTcGTcGtCAaCTGTTTACcTtT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	306 CTCTCCcAGGCGCCcCTGGACGACGCAaGaCTGCAaTTGTTCTATCTATCCcGGCCATATA
1	DK7	306 CTCTCCcAGGCGCCCACTGGACGACGCAaGGCTGCAaTTGTTCTATCTATCCcGGCCATATA
8	S11	306 CTCTCCcAGcAGCCCACTGGACGACGCAgGGCTGCAaTTGTTCTATCTATCCCGGCCATATA
4	DR4	306 CTCTCCcAGGCaCCACTGGACAACGCAAGACTGCAaTTGTTCTATCTATCCCGGCCATATA
3	DR1	306 tCTCTCCcAGGCGCCCACTGGACAACGCAAGACTGCAaTTGTTCTATCTATCCCGGCCATATA
2	DK9	306 CTCCCCAGcAGCCCACTGGACAACGCAAGACTGCAaCTGTTCTATCTATCCCGGCCATAtT
6	S18	306 CTCCCCcAGGCGCCCACTGGACAACGCAAGACTGCAaCTGTTCTATCTATCCCGGCCATATA
7	SW1	306 CTCCCCcAGGCGCCCACTGGACAACGCAAGACTGtAACTGTTCTATCTATcCCGGCCAcATA
1-8	consensus	cTCTcCCCAGcGgCCaCTGGACAaCGCAaGaCTGcAAtTGTTCtATCTAtCCcGGCCATATA

FIGURE 1A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	367 ACGGGTCatCGCATGGCaTGGGATATGATGATGAACTGGTCCCCCTACgACGGCaCTGGTAG
1	DK7	367 ACGGGTCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCCTACcACGGCGTTGGTAG
8	S11	367 ACGGGTCACCGCATGGCaTGGGATATGATGATGAACTGGTCCCCCTACgCGGCGTTGGTGg
4	DR4	367 ACGGGcCACCGCATGGCgTGGGATATGATGATGAACTGGTCCCCCTACgACACGGCTGGTAG
3	DR1	367 ACGGGaCACCGtATGGCaTGGGATATGATGATGAACTGGTCCCCCTACgACACGGCTGGTAA
2	DK9	367 ACGGGTCatCGcATGGCgTGGGATATGATGATGAACTGGTCCCCCTACgCAGCGCTGGTAA
6	S18	367 ACGGGTCACCGtATGGCATGGGATATGATGATGAACTGGTCCCCCTACAACgCGcTGGTAA
7	SW1	367 ACGGGTCACCGcATGGCATGGGATATGATGATGAACTGGTCCCCcACAACaCGcTGGTAG
1-8	consensus	ACGGGTCaCcgCATGGCaTGGGATATGATGATGAACTGGTCCCCCTACgAcCGcTGGTAG

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	428 TAGCTCAGCTGCTCCGGATCCCaAAGCCATCTTTGGAtATGATCGCTGGTGCTCACTGGGG
1	DK7	428 TAGCTCAGCTGCTCCGGATCCCGAAGCCATCTTTGACATGATCGCTGGTGCTCACTGGGG
8	S11	428 TAGCTCAGCTGCTCCGGATCCCaAAGCCATCTTTGACATGATCGCTGGTGCTCACTGGGG
4	DR4	428 TAGCTCAGCTGCTCCGGATCCCaAAGCCATCTTTGACATGATCGCTGGTGCCCACTGGGG
3	DR1	428 TGGCTCAGCTGCTCCGGATCCCaAAGCCATCTTTGACATGATCGCTGGaGCCCACTGGGG
2	DK9	428 TGGCGCAGCTGCTCAGGATCCCGCAgGCCATCTTTGACATGATCGCTGGTGCCCACTGGGG
6	S18	428 TAGCTCAGCTGCTCAGGtCCCGCAAGCCGCTTTGGACATGATCGCTGGTGCCCACTGGGG
7	SW1	428 TAGCTCAGCTGCTCAGGaTCCCGCAAGCCGCTTTGGACATGATCGCTGGTGCCCACTGGGG
1-8	consensus	TAGCTCAGCTGCTcGGaTCCC-CaAGCCATCTTTGGAcATGATCGCTGGtGCCaCTGGGG

<u>SEQ ID NO:</u>	<u>Isolate</u>	
5	S14	489 AGTCCTaGCGGGCATAGCGTATTTtTCCATGGTGGGaAACTGGGCGAAGGTCTTaGTgGTG
1	DK7	489 AGTCCTgGCGGGCATAGCGTATTTtTCCATGGTGGGGAaCTGGGCGAAGGTCTTGGTAGTG
8	S11	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGGAaCTGGGCGAAGGTCTTGGTAGTG
4	DR4	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGGAaCTGGGCGAAGGTCTTGGTAGTG
3	DR1	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGGAaCTGGGCGAAGGTCTTGGTAGTG
2	DK9	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGTGGGGAaCTGGGCGAAGGTCTTGGTAGTG
6	S18	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGcGGGGAaCTGGGCGAAGGTCTTGGTAGTG
7	SW1	489 AGTCCTAGCGGGCATAGCGTATTTtTCCATGGtGGGGAaCTGGGCGAAGGTCTTGGTAGTG
1-8	consensus	AGTCCTaGCGGGCATAGCGTATTTtTCCATGGtGGGgAACTGGGCGAAGGTCTTgGTaGTg

FIGURE 1B

SEQ ID NO:	Isolate	
11	DK1	1 TATGAAGTGCgCAACGTGTCCGGGGTGTACCaGTcACaAACGACTGCTCCAACtCAAGCA
24	T10	1 TATGAAGTGCgCAACGTGTCCGGGaTGTACCaTGTcACgAACGACTGCTCCAACtCAAGCA
10	D3	1 TATGAAGTGCgCAACGTGTCCGGGGTGTACCaAGTcACcAAtGACTGTtCCAACtCGAGCA
9	D1	1 TATGAAGTGCgCAACGTGTCCGGGGTGTACCATGTcACGAACGACTGTtCCAACtCGAGCA
14	HK5	1 TATGAAGTGCgCAACGTGTCCGGGGTATACCATGTcACGAACGACTGCTCCAACtAAGCA
15	HK8	1 TATGAAGTGCgCAACGTGTCCGGGATATACCATGTcACGAACGACTGCTCCAACtCAAGCA
12	HK3	1 TATGAAGTGCgCAACGTGTCCGGGATATACCATGTcACGAACGACTGCTCCAACtCAAGcg
23	T3	1 TAcGAAGTGCgCAACGTGTCCGGGGTGTAcTATGTcACGAACGACTGTtCCAACtCAAGCA
22	SW2	1 TATGAAGTGCgCAACGTGTCCGGGGTGTAcTATGTcACGAACGACTGTtCCAACtCAAGCA
17	IND8	1 TATGAAGTGCgCAACGTGTCCGGGGTGTACCATGTcACGAACGACTGCTCCAACtCAAGTA
16	IND5	1 TATGAAGTGCgCAACGTGTCCGGGGTGTACCATGTcACGAACGACTGCTCCAACtCAAGTA
21	SA10	1 TATGAAGTGCgCAACGTGTCCGGGaTGTACCATGTcACGAACGACTGCTCCAACtCAAGCA
20	S45	1 TATGAAGTGCgCAACGTGTCCGGGGcGTACCATGTcACGAACGACTGCTCCAACtCAAGCA
25	US6	1 TATGAAGTGCgCAACGTGTCCGGGATGTACCATGTcACGAACGACTGCTCCAACtCAAGCA
13	HK4	1 cATGAAGTGCaCAACGTaTCCGGGATcTACCATGTcACGAACGACTGCTCCAACtCAAGTA
18	P10	1 TATGAAGTGCgCAACGTgTCCGGGGTGTACCATGTcACGAACGACTGCTCCAACtCAAGTA
19	S9	1 TATGAAGTGCgCAACGTaTCCGGGGcGTACCATGTcACGAACGACTGCTCCAACtCAAGTA
9 - 25	consensus	tAtGAaGTGcGCAACGTgTCCGGGGtgTAccAtGTCACgAAcGACTGcTCCAACtCaAGCa

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	123 GaaCAACcaCTCCCGtTGCTGGGTAGCGCTCACcCCCAcGCTCGCGGCCAGGAACgCCAGC
24	T10	123 GGgCAACTCCTCCCGTGCTGGGTAGCGCTCACTCCCAcGCTCGCGGCCAGGAACACCAGC
10	D3	123 GGACAACCTCCTCTCGCTGCTGGGTAGCGCTCACCCCAcGCTCGCGGCTAGGAATAGCAGC
9	D1	123 GGACAACCTCCTCTCGCTGCTGGGTAGCGCTCACCCCAcGCTCGCGGCTAGGAATGGCAaC
14	HK5	123 aAACAACTCCTCCCGTTGtTGGGTAGCGCTCgCCCCCAcGCTCGCGGCCAGGAACgCcCAGC
15	HK8	123 GAAcAACTCCTCCCGTTGtTGGGTgCGGCTCACTCCCAcGCTCGCGGCTAGGAAtGTCAGC
12	HK3	123 GAAcAACTCCTCCCGTGtTGGGTAGCGCTCACTCCCAcGCTCGCGGCCAGGAACGTCAGC
23	T3	123 GAgCAAtTCCTCCCGTGCTGGGTAGCGCTtACTCCCAcGCTCGCGGCCAGGAACGCCAGC
22	SW2	123 GGcCAACTCCTCCCGTGCTGGGTAGCGCTCACTCCCAcGCTaGCaGCCAGGAACaCCAGC
17	IND8	123 GGGCAACTtCTCTaGtTGCTGGGTAGCGCTCACTCCCACTCTCGCGGCTAGGAACGCCAGC
16	IND5	123 GGGCAACTCCTCTCGCTGCTGGGTAGCGCTCACTCCCACTCTCGCGGCCAGGAACGCCAGC
21	SA10	123 GAAcAACTCCTCCCGTGCTGGGTAGCGCTCACTCCCAcGCTCGCGGCCAGGAATCCAGC
20	S45	123 GAAcAACTCCTCCCGtTGCTGGGTgCGGCTCACTCCCAcGCTCGCGGCCAGGAATCCAGC
25	US6	123 GAAcAACTCCTCCCGTGCTGGGTAGCGCTCACTCCCAcGCTCGCGGCCAGGAACGtLAGC
13	HK4	123 GAAcAACTCCTCCCGtTGCTGGGTAGCGCTCACTCCCAcGCTCGCGGCCAGGAACGCCAGC
18	P10	123 GAAcAACTCCTCCCGTGCTGGGTAGCGCTCACTCCCAcGCTCGCGGCTAGGAAttCCAGC
19	S9	123 GggTAACTCCTCCCAaTGCTGGGTgCGGCTCACcCCCAcGCTCGCGGCCAGGAACgCtACc
9 - 25	consensus	gaacAActcCTCcggTGcTGGGTaGCGTCaCTCCCAcGCTCGCgGCCAGGAACgcccAgC

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	184 aTCCCCACTACGACaATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
24	T10	184 GTCCCCACTACGACgATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
10	D3	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
9	D1	184 GTCCCCACTACGGCgATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
14	HK5	184 GTCCCCAcACGGCAATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
15	HK8	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
12	HK3	184 GTCCCCACcACGACaATACGACGTCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
23	T3	184 GTCCCCACTAaGACaATACGACGTCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
22	SW2	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
17	IND8	184 GTCCCCACCACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
16	IND5	184 GTctCCACCACGACaATACGACaCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
21	SA10	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
20	S45	184 GTCCCCACTACGACaATACGACGtCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
25	US6	184 GTCCCCACTACGACaATACGACGCCACGTGCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
13	HK4	184 aTCCCCACTACGACaATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
18	P10	184 GTCCCCaACTACGgCAATACGACGCCATGTCGATTGCTCGTTGGGGCGGCTGCTTCTGCT
19	S9	184 GTCCCCACcACGaCAATACGACGtCATGTCGATTGCTCGTTGGGGCGGCTGtTCTGCT
9-25	consensus	gTCCcCcAcTAcGaCaATACGACgcCAcGTGCAtTTGCTCGTTGGGGCGGCTgetTTCGct

FIGURE 1B

SEQ ID NO:	Isolate	
11	DK1	245 CCGCTATGTACGTGGGGGACCTCTGCGGATCgTTTTCCTCGTCTCTCAGCTGTTACACCTT
24	T10	245 CCGCTATGTATGTGGGAGACCTCTGCGGATCTGTTTTCCTCGTCTCTCAGCTGTTACACCTT
10	D3	245 CCGCCTATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTCGTCTCCAGCTGTTACACCTT
9	D1	245 CCGCCTATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTCaTCTCCAGCTGTTACACCTT
14	HK5	245 CCGCTATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTCGTCTCCAGCTGTTACACCTT
15	HK8	245 CCGCTATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTCGTCTCCAGCTGTTACACCTT
12	HK3	245 CCGCTATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTcGTCTCCAGCTGTTACACCTT
23	T3	245 CCGCTATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTCGTCTCCAGCTGTTACCTTT
22	SW2	245 CCGcTAATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTCGTCTCCAGCTGTTACCTTT
17	IND8	245 CCGCTATGTACGTGGGGGATCTcTGCGGATCTGTTTTCCTcGTCTCCAGCTGTTACACCTT
16	IND5	245 CCGCTATGTACGTGGGGGATCTaTGCGGATCTGTTTTCCTcGTCTCCAGCTGTTACACCTT
21	SA10	245 CCGCcaTGTACGTGGGGGAcCTcTGCGGATCTGTTTTCCTTGCTCTCCAGCTGTTACACCTT
20	S45	245 CCGCTATGTACGTGGGGGAcCTcTGCGGATCTGTTTTCCTTGTeTCCAGCTGTTACACCTT
25	US6	245 CCGCTATGTACGTGGGGGAcCTcTGCGGgTCcGTTTTCCTCaTCTCCAGCTGTTACACCTT
13	HK4	245 CCGCcaTGTACGTGGGgATCTcTGCGGATCTGTcTTCCTCGTCTCCAGcTGTTACACCTT
18	P10	245 CCGCTATGTACGTGGGGGATCTcTGCGGATCTGTTcTTCCTCGTCTCCAGCTGTTACACCTT
19	S9	245 CCGCTATGTACGTGGGGGAcTgTGCGGATCTGTTcTTCCTCaTCTCCAGCTGTTACCaT
9 - 25	consensus	CCGcTAATGTACGTGGGGgATCTcTGCGGATcTGTtTCCTcGTcTCcCAGcTGTTACAcTtT

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	306 tTCaCCTCGCCGGCATGAGACagcaCAGGACTGCAACTGCTCAATCTATCCCGGCCacgTt
24	T10	306 CTCGCCTCGCCGGCATGAGACTtTgCAGGACTGCAACTGCTCAATCTATCCCGGCCatcTG
10	D3	306 CTCGCCTCGCCGGCATGAGACaGTAcAGGAaTGTAAGTCTCAATCTATCCCGGCCACGTG
9	D1	306 CTCGCCTCGCCGGCATGAGACGGTAcAGGAgTGTAAtTGCTCAATCTATCCCGGCCACGTG
14	HK5	306 CTCGCCTCGCCGACACGAGACGGTAcAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
15	HK8	306 tTCGCCTCGCCGACACGAGACGGTAcAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
12	HK3	306 CTCGCCTCGCCGACACGAGACAGTAcAGGACTGCAACTGCTCAcTCTATCCCGGCCACGTA
23	T3	306 CTCGCCTCGCCGGCAtgAGACAGTAcAGGACTGCAACTGCTCAATCTATCCCGGCCACGTA
22	SW2	306 tTCACCTCGCCGGCacGAGACAGTAcAGGACTGCAACTGtTCCATCTATCCCGGCCACGTA
17	IND8	306 CTCACCGCGCCGGCATGAGACAGTAcAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
16	IND5	306 CTCACCGCGCCGGCATGAGACAGTAcAGGACTGCAATTGCTCCATCTATCCCGGCCACGTA
21	SA10	306 CTCGCCTCGCCGGtATGAGACAGTAcAGGACTGCAATTGCTCAATCTATCCCGGCCgCGTA
20	S45	306 CTCGCCTCGTCGGCATGAGACAGTAcAGGACTGCAAcTGTTCAATCTATCCCGGCCACGTA
25	US6	306 CTCGCCTCGTCaGCAATGAGACAGTAcAGGACTGCAATTGTTCAATCTATCCCGGCCACGTA
13	HK4	306 CTCGCCTCGCCGGCATGAGACgTACAGGACTGCAATTGcTCAATCTATCCCGGCCACGTA
18	P10	306 CTCaCCTCGCCGGCAttgGACAGTAcAGGACTGCAATTGtTCAATCTATCCtGGCCAAGTA
19	S9	306 CTCgCCcCGtCGGCATgaGACAGTACAGaACTGCAATTGcTCAATCTATCCcGGaCACGTg
9 - 25	consensus	cTCgCCtCGcCggcatgaGACagtaCAGgActGcAAcTGcTcaATCTATCCcGGcCacgTa

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCaCCTACAACAGCCTAGTgc
24	T10	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCGCCTACAACAGCCTAGTGG
10	D3	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCTACaCAGCCCTAGTGG
9	D1	367 ACAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCtTAGTGG
14	HK5	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAACAGCCCTAGTGG
15	HK8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCcACAACAGCCCTAGTGG
12	HK3	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCcCtACaCAGCCCTAGTGG
23	T3	367 aCAGGTCACCGtATGGCTTGGGATATGATGATGAACTGGTCgCCcACAaCgGCaTAGTGG
22	SW2	367 TCAGGTCACCGCATGGCTTGGGAcATGATGATGAACTGGTCACCTACAGCaGCCCTgGTGG
17	IND8	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCgGCCCTAGTGG
16	IND5	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
21	SA10	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACaCAGCCTAGTAg
20	S45	367 ACAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCgCCtACAGCAGCCTTAGTGG
25	US6	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAaTGGTCACCTACAGCAGCCCTAGTGG
13	HK4	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCACCTACAGCAGCCCTAGTGG
18	P10	367 TCAGGTCACCGCATGGCTTGGGATATGATGATGAACTGGTCGCCcACAGCAGCCCTAGTGG
19	S9	367 aCAGGTCatCGCATGGCtTGGGATATGATGATGAACTGGTCGCCtACAaCAGCCCTAGTGG
9-25	consensus	tCAGGTCaCgCATGGCtTGGGATATGATGATGAaCTGGTCaCCTACAaCAGCCTcTaGTgg

FIGURE 1B

SEQ ID NO:	Isolate	
11	DK1	428 TaTCGCAGTTACTCCGaATCCCAAGCTGTCgTGGACATGGTgGcGGGGCCCACTGGGG
24	T10	428 TgTCGCAGTTACTCCGGATCCCAAGCTGTCaTGGACATGGTgaCaGGGGCCCACTGGGG
10	D3	428 TATCGCAGTTACTCCGGATCCCAAGCTGTCgTGGACATGGTGGCGGGGGCCCACTGGGG
9	D1	428 TATCGCAGTTACTCCGGATCCCAAGCTGTCaTGGACATGGTGGCGGGGGCCCACTGGGG
14	HK5	428 TGTTCGCAGTTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTaGCGGGGGCCCACTGGGG
15	HK8	428 TGTTCGCAGTTACTCCGGATCCCGCAAGCTaTCGTGGACATGGTGGCGGGGGCCCACTGGGG
12	HK3	428 TGTTCGCaATTACTCCGGATCCCGCAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
23	T3	428 TGTTCGCAGTTgCTCCGGATCCCAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
22	SW2	428 TATCGCAGTTaCTCCGGATCCCAAGCTGTCGTGGACATGGTaGCGGGGGCCCACTGGGG
17	IND8	428 TATCGCAGTTGCTCCGGATCCCAAGCTGTCGTGGATATGGTGGCGGGGGCCCACTGGGG
16	IND5	428 TATCGCAGTTGCTCCGGATCCCAAGCTGTCGTGGATATGGTGGCGGGGGCCCACTGGGG
21	SA10	428 TATCGCAGTTACTCCGGATCCCAAGCTaTCGTGGACATGGTGGCGGGGGCCCACTGGGG
20	S45	428 TATCGCAGTTACTCCGGATCCCAAGCTGTCGTGGACATGGTGGCGGGGGCCCACTGGGG
25	US6	428 TATCGCAGTTACTCCGGATCCCAAGCTGTaTGGACATGGTGGCGGGGGCCCACTGGGG
13	HK4	428 TATCGCAGTTACTCCGaCTCCCAAGCTGTaTGGACATGGTGGCGGGGaGCCCCACTGGGG
18	P10	428 TgTCGCAGCTACTCCGGATCCCAAGCTaTCTGGATgTGGTGGCGGGGGCCCACTGGGG
19	S9	428 TaTCGCAGCTACTCCGGATCCCAAGCTgTCaTGGATaTGGTGGCGGGGGCCCACTGGGG
9-25	consensus	TaTCGCAGtTaCTCCGgaTCCCaCAAGCTgTCgTGGAcATGGTgGcGgGgGCCCACTGGGG

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	489 AGTCCTGGCGGGCCTcGCCTACTAcTCCATGGCGGGGAAC TGGGcAAGGTtTTAATTGTG
24	T10	489 AGTCCTGGCGGGCCTcGCCTACTATTCCATGGCGGGGAAC TGGGCTAAGGTtTTAATTGTG
10	D3	489 GGTCTTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTTGATTGTG
9	D1	489 GGTCTTGGCGGGCCTCGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTTGATTGTG
14	HK5	489 GGTCTTGGCGGGCCTTGcCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTTGATTGTG
15	HK8	489 AGTCCTAGCGGGCCTTGcCTACTATTCCATGGTGGGcAAC TGGGCTAAGGTtTTTGATTGTG
12	HK3	489 AGTCCTAGCGGGCCTTGcCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTTGATTGTG
23	T3	489 AGTCCTGGCGGGCCTTGcCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTTGATTGTG
22	SW2	489 AGTCCTGGCGGGCCTTGcTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTTGATTGTG
17	IND8	489 AATCCTGGCGGGCCTTGcCTACTATTCCATGGTAGGGAAC TGGGCTAAGGTtTTTGATTGTG
16	IND5	489 AATCCTGGCGGGCCTTGcCTACTATTCCATGGTAGGGAAC TGGGCTAAGGTtTTTGATTGTG
21	SA10	489 AGTCCTAGCGGGCCTTGcCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTTGATTGTt
20	S45	489 AGTCCTGGCGGGCCTTGcCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTCTGATTGTG
25	US6	489 AGTCCTGGCGGGCCTTGcCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTCTGATTGTG
13	HK4	489 AGTCCTAGCGGGCCTTGCtTACTATTCCATGGTGGGGAAC TGGGcCAAGGTtTTTGATTGTG
18	P10	489 AGTCCTGGCGGGCCTTGcCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTCTGATTGTG
19	S9	489 AGTCCTGGCGGGCCTcGCCTACTATTCCATGGTGGGGAAC TGGGCTAAGGTtTTGATTGTG
9-25	consensus	agTCCTgGCGGGCCTtGCcTACTAtTCCATGGtgGgGAAC TGGGcTAAGGTtTgATTGTg

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
11	DK1	550 tTGCTACTCTTTGCGCGGTtGATGGG
24	T10	550 ATGCTACTCTTTGCGCGGTtGATGGG
10	D3	550 ATGCTACTCTTTGCTGGCGTcGACGGC
9	D1	550 ATGCTACTCTTTGCTGGCGGTtGACGGC
14	HK5	550 ATGCTACTtTTTGCGCGGTtGATGGG
15	HK8	550 ATGCTACTgTTTGCGCGGTtGATGGG
12	HK3	550 ATGCTACTtTTTGCGCGGTtGATGGG
23	T3	550 cTGCTACTCTTTGCGCGGTtGATGGG
22	SW2	550 ATGCTACTCTTTGCTGGCGGTtGACGGG
17	IND8	550 ATGCTACTCTTTGCGCGGTtGACGGG
16	IND5	550 ATGCTACTCTTTGCGCGGTtGACGGG
21	SA10	550 ATGCTACTCTTTGCGCGGTtGACGGG
20	S45	550 ATGCTACTCTTTGCGCGGTtGACGGG
25	US6	550 tTGCTACTCTTTGCGCGGTtGACGGG
13	HK4	550 ATGCTACTCTTTGCGCGGTtGACGGG
18	P10	550 ATGCTACTCTTTGCGCGGTtGACGGa
19	S9	550 ATGCTACTtTTTGCTGGtGTTGACGGg
9-25	consensus	aTGCTACTcTTTGCCGGcGTtGAcGGg

FIGURE 1C

SEQ ID NO: Isolate

26 T2

27 T4

28 T9

29 US10

26-29 consensus

1 GCcCAAGTGAAGAACACCAGccgCgGtTACATGGTGACTAACGACTGTTCCaATGAgAGCA

1 GCaCAAGTGAAGAACACCacTaaCAGCTACATGGTGACCaaCAGACTGTTCTaATGACAGCA

1 GCCgAAGTGAAGAACACCAGTACCAGCTACATGGTGACAaATGACTGTTCCaACGACAGCA

1 GtCcAAGTGAaaAACACCAGTACCAGCTAtATGGTGACCaaATGACTGCTCCaACGACAGCA

GcccAAGTGAagAACACCAGtacCaGcTAcATGGTGACCaa-GACTGtTCCaa-GAcAGCA

SEQ ID NO: Isolate

26 T2

27 T4

28 T9

29 US10

26-29 consensus

62 TCACcTGGCAGCTCCAaGCCGCGGtCTCCACGTCCCCGGGTGTaTCCCGTGtGAGAggct

62 TCActTGGCAGCTCCAGGCCGCGGTCCTCCACGTCCCCGGGTGTGTCCCGTGCGGAGaaAac

62 TCACcTGGCAACTCCAGGCCGCGGTCCTCCACGTCCCCGGGTGcGTCCCGTGCGGAGAgGT

62 TCActTGGCAACTtgAGGCTcGCGTCCTCCACGTcCCCCGGGTGcGTCCCGTGCGGAGaaGT

TCAC-TGGCA-CTccAgGcCcGGGTcCTCCACGTcCCCCGGGTGtGTCCCGTGcGAGA-agt

SEQ ID NO: Isolate

26 T2

27 T4

28 T9

29 US10

26-29 consensus

123 GGGAAATACATCtCGaTGCTGGATACCGGTcaCACCAAACGTGGCCGTGCGGCAGCCCGGC

123 GGGAAATACATCtCGGTGCTGGATACCGGTtTCAACCAAACGTGGCCGTGCGGCAGCCCGGC

123 tGGAAAcgCgTCgCGGTCTGGATACCGGTCTCgCCAAACGTaGctGTGCAGCGGCTGGC

123 gGGAAAtaCaTCTcGGTGTGGATACCGGTCTCaCAAAtGTgGCcGTGCAGCGGCTGGC

gGGAAAtaCaTCTcGGTGTGGATACCGGTtCaCAAACGTgGCcGTGC-GC-GCC-GGC

SEQ ID NO: Isolate

26 T2

27 T4

28 T9

29 US10

26-29 consensus

184 GCtCTtACGCAGGGCTTGCGGACGCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT

184 GCCCTCACGCAGGGCTTGCGGACGCACATtGACATGGTtGTGATGTCCGCCACGCTCTGCT

184 GCCCTCACGCAGGGCTTGCGGACGCACATCGACATGGTtGTGATGTCCGCCACGCTCTGCT

184 GCCCTCACGCAGGGCTTGCGGActCACATCGACATGGTcGTGATGTCCGCCACGCTCTGCT

GCcCTcACGCAGGGCTTGCGGAcgCACATcGACATGGTtGTGATGTCCGCCACGCTCTGCT

SEQ ID NO: Isolate

26 T2

27 T4

28 T9

29 US10

26-29 consensus

245 CTGCcCTcTACGTGGGGGACCTCTGCGCGGGGTGATGTCTCGCAGCCAGATGTTcATtGT

245 CTGCTCTtTACGTGGGGGACCTCTGCGCGGGGTGATGTCTCGCAGCCAGATGTTcATcGT

245 CCGCTCTcTACGTGGGGGActCTCTGCGCGGGGTaATGTCTCGcGCTcAGATGTTcATTaT

245 CCGCTCTtTACGTGGGGGActCTCTGCGGtGGGaTgATGTCTCGCaGcCaAaTGTTCATTgT

C-GCTCT-TACGTGGGGGAcCTCTGCGCGGGGTgATGTCTCGCaGcCaGATGTTcATTgT

FIGURE 1C

<u>SEQ ID NO:</u>	<u>Isolate</u>	
26	T2	306 CTGCGCGcACgCCTACTGGTTTGTGCAAGAAATGCAATTGCTCtATCTACCCcGGtACCATC
27	T4	306 CTGCGCGCAACatCACTGGTTTGTGCAAGAcTGCAATTGCTCtATCTACCCtGGcACCATC
28	T9	306 CTGCGCGCagCACCACTGGTTTGTGCAGGAATGCAACTGCTCCATtTACCCTGGTACCATC
29	US10	306 CTGCGCGgcCACCACTcGTTTGTGCAGGAATGCAACTGCTCCATcTACCcGGTACCATC
26-29	consensus	CTGCGCGC-aCacCACTgGTTTGTGCA-GAATGCAA-TGCTCcatCTACCC-GGtACCATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
26	T2	367 ACTGGACACCGTATGGCATGGGAcATGATGATGAACtGGTCGCCcACaGCCACCATGATCC
27	T4	367 ACTGGACACCGTATGGCATGGGAcATGATGATGAACtGGTCGCCcACgGCCACCATGATCC
28	T9	367 ACTGGACACCGTATGGCATGGGACATGATGATGAACtGGTCGCCcACaCCACCATGATCt
29	US10	367 ACcGgGcCACCGTATGGCATGGGACATGATGATGAACtGGTCGCCcACgGCACctTGATCc
26-29	consensus	ACTGGACACCGTATGGCATGGGAcATGATGATGAACtGGTCGCCcAC-gCCACcatGATCc
<u>SEQ ID NO:</u>	<u>Isolate</u>	
26	T2	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCATCaTAGACATCaTcgGCGGGGctCACTGGGG
27	T4	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCATCtTAGACATCgTLAGCGGGGCaCACTGGGG
28	T9	428 TGGCGTACGCGATGCGCGTTCCCGAGGTCATCATAGACATCATcAGCGGaGctCACTGGGG
29	US10	428 TGGCGTACgTGATGCGCGTTCCCGAGGTCATCATAGACATCATcLAGCGGgGcGcatTGGGG
26-29	consensus	TGGCGTACGcGATGCGCGTTCCCGAGGTCATCaTAGACATCaT-aGCGGgGctCAcTGGGG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
26	T2	489 CGTCATGTTtGGCTTGGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAgGTCaTTGTCATC
27	T4	489 CGTCATGTTTCGGCTTGGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAaGTCGTTGTCATC
28	T9	489 CGTCATGTTTCGGCctTAGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAgGTCGTTGTCATC
29	US10	489 CGTcTtGTTTCGGctTAGCCTACTTCTCTATGCAGGGAGCGTGGGCGAAaGTCGTTGTCATC
26-29	consensus	CGTCaTGTTtGGctT-GCCTACTTCTCTATGCAGGGAGCGTGGGCGAA-GTCgTTGTCATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
26	T2	550 CTctTGCTGGctGCTGGGGtGGACGCG
27	T4	550 CTctTGCTGGcCGCTGGGGtGGACGCG
28	T9	550 CTgtTGCTcAcCGCTGGcGTGGACGCG
29	US10	550 CTtctTGCTagCGCTGGgGTGGACGCG
26-29	consensus	CTt-TGCTggCcGCTGGgGTGGACGCG

FIGURE 1D

<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	1 GTGGAAGTLAGAAACaCAGTTtAGCTACTACGCCACCAATGATTGCTCgAAACAACAGCA
30	DK8	1 GTGGAAGTCAGGAACATCAGTTTCAGCTACTACGCCCAACCAATGATTGCTCAAAACAACAGCA
32	SW3	1 GTGGAAGTCAGGAACATCAGTTTCAGCTACTAtGCCACCAATGATTGCTCAAAACagCAGCA
31	DK11	1 GTGGAAGTCAGGAACaCAGTTTCAGTtACTAcGCCCAACCAATGATTGCTCAAAACAaCAGCA
30-33	consensus	GTGGAAGTcAGgAAcA - CAGTTtAGcTACTAcGCCCAACCAATGATTGCTCAAAACAaCAGCA
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	62 TCACCTGGCagCTCACCaaCGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
30	DK8	62 TCACCTGGCACTCACCgACGCAGTTCTCCACCTTCCCGGATGCGTCCCATGTGAGAATGA
32	SW3	62 TCACCTGGCACTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCcGTGTGAGAATGA
31	DK11	62 TCACCTGGCACTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCaATGTGAGAATGA
30-33	consensus	TCACCTGGCAaCTCACCaaCGCAGTtCTCCACCTTCCCGGATGCGTCCaATGTGAGAATGA
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	123 CAATGGCACCCtTGCGCTGCTGGATACAAGTaaCACCTAAATGTGGCTGTGAAACACCGcGGC
30	DK8	123 CAATGGCACCCCTGCGCTGCTGGATACAAGTgACACCTAAATGTGGCTGTGAAACACCGCGGC
32	SW3	123 CAATGGCACCCCTGCACTGCTGGATACAAGTgACACCTAAATGTGGCTGTGAAACACCGCGGC
31	DK11	123 CAATGGCACCCCTGCACTGCTGGATACAAGTgACACCTAAATGTGGCTGTGAAACACCGCGGC
30-33	consensus	CAATGGCACCCtTGC - CTGCTGGATACAAGTgACACCTAAATGTGGCTGTGAAACACCGcGGC
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	184 GCACTcACTCaaAACCTGCGAAcGCaTgTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
30	DK8	184 GCACTtACTCAtAACCTGCGAAcACAGCTCGACGTGATCGTAATGGCAGCTACGGTCTGCT
32	SW3	184 GCgCTCACTCaaAACCTGCGAGcACAGCTCGATATGATCGTAATGGCAGCTACGGTCTGCT
31	DK11	184 GCaCTCACTCaaAACCTGCGAGcACaTaGATATGATtGTAATGGCAGCTACGGTCTGCT
30-33	consensus	GCaCTcACTCaaAACCTGCGA - CaCA - gTcGA - - TGATcGTAATGGCAGCTACGGTCTGCT
<u>SEO ID NO:</u>	<u>Isolate</u>	
33	T8	245 CGGCCCTTGATGTGGGgGACGTgTgCGGGGGCCGTGATGATAgcGTCGAGGCTtTCATAAT
30	DK8	245 CGGCCCTTGATGTGGGAGACGTaTgCGGGGGCCGTGATGATCGTGTGCGAGGCTcTCATAAT
32	SW3	245 CGGCCCTTGATGTGGGAGACaTgTgCGGGGGCCGTGATGATCGTGTGCGAGGCTtTCATAAT
31	DK11	245 CGGCCCTTGATGTGGGAGACgTgTgCGGGGGCCGTGATGATCGTGTGCGAGGCTtTCATAgT
30-33	consensus	CGGCCCTTGATGTGGGgGACgTgTgCGGGGGCCGTGATGATcGtGTCGAGGCTtTCATAaT

FIGURE 1D

<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	306 ATCGCCaGAACGCCaCAACTTcACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
30	DK8	306 ATCGCCTGAACGCCaCAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCATATC
32	SW3	306 ATCGCCAGAAGGCCaCAACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCgTATC
31	DK11	306 ATCGCCAGAACaCCACcACTTTACCCAGGAGTGCAACTGTTCCATCTACCAAGGTCaCATC
30-33	consensus	ATCGCCaGAACGCCaCAACTTcACCCA-GAGTGCAACTGTTCCATCTACCAAGGTCatATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTgAACTGGTCACCAACTCTcACCATGATCC
30	DK8	367 ACCGGCCACCGCATGGCATGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
32	SW3	367 ACCGGCCACCGCATGGCgTGGGACATGATGCTAAACTGGTCACCAACTCTTACCATGATCC
31	DK11	367 ACCGGCCACCGCATGGCaTGGGACATGATGCTLAACTGGTCACCAACTCTcACCATGATCC
30-33	consensus	ACCGGCCACCGCATGGCaTGGGACATGATGCTAACTGGTCACCAACTCTc-ACCATGATCC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	428 TCGCCTAcGctGCTCGTGtGCTTGAACTAGtCCCTtgAaGTTGTCTTCGGCGGCCATTGGGG
30	DK8	428 TCGCCTATGCCGCTCGTGTTCTTGAGCTAGcCCTtcAgGTTGTCTTCGGCGGCCATTGGGG
32	SW3	428 TcGCTATGCCGCTCGTGTTCTTGAGCTAGTCTTGAAAGTTGTCTTCGGCGGCCATTGGGG
31	DK11	428 TcGCTATGCCGccCGTGTTCTTGAGCTAGTCTTGAAAGTcGTCTTCGGtGGtCATTTGGGG
30-33	consensus	TcGCTATcGCcGctCGTGtTCTTGAGCTAGtCCCTtgAaGtTGTCTTCGGcGGcCATTGGGG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	489 CGTGGTGTtTGGCTTGGCCTATtTCTCCATGCAaGGAGCGTGGGCCAAAGTCATcGCCATC
30	DK8	489 CGTGGTGTtTGGCTTGGCCTATtTCTCCATGCAgGGAGCGTGGGCCAAAGTCATTGCCATC
32	SW3	489 CGTGGTGTtTGGCTTGGCCTATtTCTCCATGCAaGGAGCGTGGGCCAAAGGTCATTGCCATC
31	DK11	489 tGTGGTGTtTGGCTTGGCCTATtTCTCCATGCAgGGAGCGTGGGCCAAAGGTCATTGCCATC
30-33	consensus	cGTGGTGTtTGGCTTGGCCTATtTCTCCATGCA-GGAGCGTGGGCCAA- GTCATtGCCATC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
33	T8	550 CTCCTcCTTGTcGCAGGAGTGGaGCA
30	DK8	550 CTCCTcCTTGTcGCAGGAGTGGATGCA
32	SW3	550 CTCCTgCTTGTcGCAGGAGTGGATGCA
31	DK11	550 CTCCTcCTTGTaGCAGGAGTGGATGCA
30-33	consensus	CTCCTcCTTGTcGCAGGAGTGGaTGCA

FIGURE 1E

SEQ ID NO:	Isolate	
35	DK12	1 tTAGAGTGGCGGAATGTGTCcGGCCTCTAcGTCCTTACCAACGACTGTtCCAATAGCAGTA
36	HK10	1 CTAGAGTGGCGGAATGTGTCGGCCTCTATGTCTTACCAACGACTGTtCCAATAGCAGTA
37	S2	1 CTAGAGTGGCGGAATACGTCCTGGCCTCTATGTCTcACCAACGACTGTtCCAATAGCAGTA
39	S54	1 CTAGAGTGGCGGAATACGTCCTGGCCTCTATaTCCTTACCAACGACTGTtCCAATAGCAGTA
38	S52	1 CTAGAGTGGCGGAATACGTCCTGGCCTCTATgTCCTTACCAACGACTGTtCCAATAGCAGTA
35-39	consensus	cTAGAGTGGCGGAATAcGTCtGGCCTCTAtgTCCTTACCAACGACTGTtCCAATAGCAGTA
35	DK12	62 TeGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
36	HK10	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
37	S2	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
39	S54	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
38	S52	62 TTGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
35-39	consensus	TtGTGTATGAGGCCGATGACGTCATTCTGCACACACCTGGCTGTGTACCTTGTGTTcAGGA
35	DK12	123 CGGCAATACATCtACGTGCTGGACCTCaGTGACgCCTACAGTGGCAGTCAGGTACGTCGGA
36	HK10	123 CGGCAATACATCCACGTGCTGGACCTCgGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
37	S2	123 CGGCAATACATCCACGTGCTGGACCCAGTGACACCTACAGTGGCAGTCAGGTAtGTCGGA
39	S54	123 CGGCAATACATCCACGTGCTGGACCCAGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
38	S52	123 CGGCAATACATCCAtGTGCTGGACCCAGTGACACCTACAGTGGCAGTCAGGTACGTCGGA
35-39	consensus	CGGcAATACATCCAcGTGCTGGACCcCaGTGACaCCTACaGTGGCAGTCAGGTACGTCGGA
35	DK12	184 GCAACCACCGCtTCGATACGCAGTCATGTGGACCTGcTAGTGGGCGCGGCCACGATGTGCT
36	HK10	184 GCAACCACCGCcTCGATACGCAGTCATGTGGACCTGTtTAGTGGGCGCGGCCACGATGTGCT
37	S2	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTAtTgTGGGCGCGGCCACtATGTGCT
39	S54	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTAtTAGTGGGCGCGGCCACGCTGTGCT
38	S52	184 GCAACCACCGCTTCGATACGCAGTCATGTGGACCTAtTAGTGGGCGCGGCCACGCTGTGCT
35-39	consensus	GCAACCACCGCtTCGATACGCAGTCATGTGGACCTAtTAGTGGGCGCGGCCACgATGTGCT

FIGURE 1E

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	245 CTGCGCTCTACGTGGGtGATgTGtGTGGGGCCGTCTTCtCTcGTGGGACAAGCCTTCACGTT
36	HK10	245 CTGCGCTCTACGTGGGcGATATGTGTGGGGCCGTCTTCCTCGTGGGACAAGCCTTCACGTT
37	S2	245 CTGCGCTCTACGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
39	S54	245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
38	S52	245 CTGCGCTCTATGTGGGTGATATGTGTGGGGCCGTCTTTCTCGTGGGACAAGCCTTCACGTT
35-39	consensus	CTGCGCTCTAcGTGGGtGATaTGtGTGGGGCCGTCTTtCTcGTGGGACAAGCCTTCACGTT

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	306 CAGACcctCGTCGCCATCAAAcGtCCAGACCTGTAACTGCTCGCTGTACCCAGGCCatCTT
36	HK10	306 CAGACcGcGTTCGCCATCAAAcCGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCAcCTT
37	S2	306 CAGACCTCGTCGCCATCAAAcCGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
39	S54	306 CAGACCTCGTCGCCATCAAAcCGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATCTT
38	S52	306 CAGACCTCGTCGCCATCAAAcCGTCCAGACCTGTAACTGCTCGCTGTACCCAGGCCATgTT
35-39	consensus	CAGACcctCGTCGCCATCAAAcGtCCAGACCTGTAACTGCTCGCTGTACCCAGGCCatcTT

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG
36	HK10	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCcGTGGGTATGGTGG
37	S2	367 TCAGGACATCGcATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
39	S54	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
38	S52	367 TCAGGACATCGAATGGCTTGGGATATGATGATGAATTGGTCCCCCGCTGTGGGTATGGTGG
35-39	consensus	TCAGGACATCGaATGGCTTGGGATATGATGATGAATTGGTCCCCCGCtGTGGGTATGGTGG

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	428 TaGCGCACGTCCTCGGtCTGCCCCAGACCTTGTTcGACATAATAGtCGGGGCCcATTGGGG
36	HK10	428 TGCGCACGTCCTCGGgTTGCCCCAGACCTTGTTcGACATAATAGcCGGGGCCcATTGGGG
37	S2	428 TGCGCACGCTtCTCGGtTTGCCCCAGACcGTGTTcGACATAATAGCCGGGGCCcATTGGGG
39	S54	428 TGCGCACATcCTCGGATTGCCCCAGACCTTGTTTGACATACTGGcCGGGGCCcATTGGGG
38	S52	428 TGCGCACATcCTCGGATTGCCCCAGACCTTGTTTGACATACTGGcCGGGGCCcATTGGGG
35-39	consensus	TgGCGCACgTcCTCGG- tTGCCCCAGACCTTGTTcGACATAaTaGcCGGGGCCcATTGGGG

FIGURE 1B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	489 CATCaTGGCGGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
36	HK10	489 CATCTTGGCaGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
37	S2	489 CATCTTGGCGGGCCTAGCCTATTACTCCATGCaaGGCAACTGGGCCAAGGTCGCTATCATC
39	S54	489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATCATC
38	S52	489 CATCTTGGCGGGCCTAGCCTATTATTCTATGCAGGGCAACTGGGCCAAGGTCGCTATtgTC
35-39	consensus	CATCtTGGCGGGCCTAGCCTATTATCcATGCaGGCAACTGGGCCAAGGTCGCTATcaTC
<u>SEQ ID NO:</u>	<u>Isolate</u>	
35	DK12	550 ATGGTTATGTTTTTCAGGaGTCGATGCC
36	HK10	550 ATGGTTATGTTTTTCAGGGGTCGATGCC
37	S2	550 ATGGTTATGTTTTTCAGGGGTCGAcGCC
39	S54	550 ATGATTATGTTTTTCAGGGGTCGATGCC
38	S52	550 ATGATTATGTTTTTCAGGGGTCGATGCC
35-39	consensus	ATGgTTATGTTTTTCAGGgGTCGAtGCC

FIGURE 1F

<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	1 GTCAACTATCaCAATGCCTCGGGCGTCTATCACATCACCAACGACTGCCCGAACTCGAGCA
42	Z6	1 GTCAACTATCGCAATGCCTCGGGCGTCTATCACGTACCAACGACTGCCCGAACTCGAGCA
42-43 consensus (Z6)		GTCAACTATCgCAATGCCTCGGGCGTCTATCAGcTACCAACGACTGCCCGAACTCGAGCA
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	62 TAaTGTATGAGGCCGAACACCACATCCTACACCTCCCAGGGTGCCTACCTGTGTGAGGGa
42	Z6	62 TAGTGTATGAGGCCGAACACCagATCTTACACCTCCCAGGGTGCtTgCCCTGTGTGAGGGt
42-43 consensus (Z6)		TagTGTATGAGGCCGAACACCagATCTTACACCTCCCAGGGTGCtTgCCCTGTGTGAGGGt
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	123 gGGGAACcAGTCACGCTGCTGGGTGGCCCTTACTCCCAACCGTGGCGGcGcCTTATATCGGT
42	Z6	123 tGGGAAtcAGTCACGCTGCTGGGTGGCCCTTACTCCCAACCGTGGCGGtGtCTTATATCGGT
42-43 consensus (Z6)		tGGGAAtcAGTCACGCTGCTGGGTGGCCCTTACTCCCAACCGTGGCGGtGtCTTATATCGGT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	184 GCaCCGCTTGAaTCCaTCCGGAGACATGTGGACCTGATGGTAGGCGctGCTACaGTGTGCT
42	Z6	184 GCTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTGGGCGCGCTACTGTaTGCT
42-43 consensus (Z6)		GCTCCGCTTGAcTCCcTCCGGAGACATGTGGACCTGATGGTgGGCGCcGCTActGTaTGCT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	245 CcGcTCTCTACaTTGGGGACCTGTGCGGTGGcGtAItTtTTGGTGTGctCAGATGItTtCTTT
42	Z6	245 CtGCCCTCTACgTTGGAGATcGTGTGCGGTGGTGcATTtCTTGGTGTGcCAGATGtTtCTCTT
42-43 consensus (Z6)		CtGCCCTCTACgTTGGaGATcGTGTGCGGTGGtGcATTtCTTGGTGTGcCAGATGtTtCTcTT
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTCCATCTAtGcGgGGGCAcGtTt
42	Z6	306 CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTcTAtCTACGCAGGGCATATC
42-43 consensus (Z6)		CCAGCCGCGACGCCACTGGACTACGCAGGACTGCAATTGTTcTAtCTACGCAGGGCAtaTc
<u>SEQ ID NO:</u>	<u>Isolate</u>	
43	Z7	367 ACaGGCCACAGaATGGCATGGGACATGATGATGAACCTGGAGTCCCACAACCACctTGgTCC
42	Z6	367 ACgGGCCACAGgATGGCATGGGACATGATGATGAACCTGGAGTCCCACAACCACCCTGcTtC
42-43 consensus (Z6)		ACgGGCCACAGgATGGCATGGGACATGATGATGAACCTGGAGTCCCACAACCACCcTgCtTc

FIGURE 1F

SEQ ID NO: Isolate

43 Z7

42 Z6

42-43 consensus (Z6)

428 TCGCCCAGGTtATGAGGATCCCTAGCACTCTGGTgGACCTACTCaCTGGAGGGCACTGGG
 428 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTAgAtCTACTCGCTGGAGGGCACTGGG
 TCGCCCAGGTcATGAGGATCCCTAGCACTCTGGTAgAtCTACTCgCTGGAGGGCACTGGG

SEQ ID NO: Isolate

43 Z7

42 Z6

42-43 consensus (Z6)

489 taTCCTTaTcGGGgTGGCaTACTTctGCATGCAAGCTAATTGGGCCAAGGTCAttCTGGTC
 489 CgTCCTTGTTGGGtTGGCGTACTTcAGtATGCAAGCTAATTGGGCCAAaGTCATCCTGGTC
 cgTCCTTgTtGGGtTGGCgTACTTcAGtATGCAAGCTAATTGGGCCAAaGTCATcCTGGTC

SEQ ID NO: Isolate

43 Z7

42 Z6

42-43 consensus (Z6)

550 CTTTTCTCTTaCGCTGGAGTTGATGCC
 550 CTTTTCTCTTcCGCTGGAGTTGATGCC
 CTTTTCTCTTcCGCTGGAGTTGATGCC

FIGURE 1G

SEQ ID NO: Isolate

45 SA1
47 SA5
49 SA7
46 SA4
50 SA13
48 SA6
45-50 consensus

1 GTtCCCTACCGgAATGCCTCTGGGGTTTtAcCATGTcACCAATGAcTGCCCAAACTCctCCA
1 GTCCCTTACCGAAATGCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTtCCA
1 GTCCCTTACCGAAATGCCTCcGGGGTTTATCATGTcACCAATGATTGCCCGAACTCTtCCA
1 GTTCCCTACCGAAAcGCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTtCCA
1 GTTCCCTACCGAAATGCCTCTGGGGTTTATCATGTcACCAATGATTGCCCAAACTCTtCCA
1 GTTCCTtACCGgAATGCCTCTGGGGTgTATCATGTtACCAATGATTGCCCAAACTCTtCCA
GTtCCcTACCGAAAtGCCTCtGGGGTtTATCATGTcACCAATGATTGCCCAAACTCtTCCA

SEQ ID NO: Isolate

45 SA1
47 SA5
49 SA7
46 SA4
50 SA13
48 SA6
45-50 consensus

62 TAGTCTACGAGGCTGATAgCCTGATctTGcACGCACCTGGcTGCGTGCCCTGTGTcAgGcA
62 TAGTCTACGAGGCTGATAACCTGATctTGcACGCACCTGGTtGCGTGCCCTGTGTcAaGgA
62 TAGTCTAtGAGGCTGAcaACCTGATcCTGcACGCACCTGGTtGCGTGCCCTGTGTcAGaCA
62 TAGTctTACGAGGCTGATAACCTGATCTTGCAcGCACCTGGTtGCGTGCCctTGtGTcAGGCA
62 TcGTCTACGAGGCTGATGACCTGATCTTACACGCACCTGGTtGCGTGCCCTGTGTtAGGCA
62 TaGTCTAtGAGGCTGATGACCTGATCcTACACGCACCTGGcTGCGTGCCCTGTGTccGgAa
TaGTcTAcGAGGCTGATaaCCTGATc - TgCAcGCACCTGGtTGCGTGCCcTGtGTcaggcA

SEQ ID NO: Isolate

45 SA1
47 SA5
49 SA7
46 SA4
50 SA13
48 SA6
45-50 consensus

123 AGaTAATGTcAGTAGGTGCTGGGTCCAAATcACCCCCAcATGTcAGCCCCGAcCtTCGGA
123 AGgTAATGTcAGTAGGTGCTGGGTCCAAATcACCCCCAcATTGTcAGCCCCGAACCTCGGA
123 AaTAATGTcAGTAGGTGCTGGGTCCAAATcACCCCCAcATTGTcAGCCCCGAACCTCGGA
123 AGATAATGTcAGTAAgTGCTGGGTCCAAATcACCCCCAcGtTGTcAGCCCCGAATcTCGGA
123 GGGTAATGTcAGTAGGTGCTGGGTCCAgATcACCCCCAcACTGTcAGCCCCGAGCCTCGGA
123 GGAaTAATGTcAGTAGATGTCTGGGTcCATATcACCCCCAcACTATcAGCCCCGAGCCTCGGA
agaTAATGTcAGTAGgTGCTGGGTcCAaATcACCCCCAc - TgTcAGCCCCGAACCTCGGA

FIGURE 1G

SEO ID NO: Isolate

45 SA1
47 SA5
49 SA7
46 SA4
50 SA13
48 SA6
45-50 consensus

184 GCGGTACGGCTCCTCTTCGGAGGGcCGTTGACTACTTAGCGGGAGGgAGCTGCTCTCTGCT
184 GCGGTACGGCTCCTCTTCGGAGGGcCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGACTACcTAGCGGGAGGGGCTGCCCTCTGCT
184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGAGGGGCTGCCCTCTGCT
184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGACTACTTAGCGGGgGGGGCTGCCCTtTGCT
184 GCGGTACGGCTCCTCTTCGGAGGGCCGTTGATTACTTgCGGGgAGGGGcGCCCTgTGCT
GCGGTACGGCTCCTCTTCGGAGGGcCGTTGACTACTTaGCGGGgAGGGcGCTGCcCTcTGCT

SEO ID NO: Isolate

45 SA1
47 SA5
49 SA7
46 SA4
50 SA13
48 SA6
45-50 consensus

245 CCGCACTATACGTCCGcGACGCGTGCggggCAGTGTtTcTGGTAGGCCAAATGTTCACTTA
245 CCGCACTATACGTCCGGGACGCGTGCggggCAGTGTtTcTGGTAGGCCAAATGTTCACTTA
245 CCGcGTATACGTCCGGGACGCGTGCggggCAGTGTtTcTGGTAGGCCAgATGTTCAgCTTA
245 CCGcATATACGTCCGGGACGCGTGCggggCAGTGTtTcTGGTAGGCCAAATGTTCACTTA
245 CCGCGTTATACGTCCGAGACGCGTGCggggCAGTGTtTcTGGTAGGcCAAATGTTCACTTA
245 CCGCGTTATACGTCCGAGACGcGTGCggggCAcTGTtTcTGGTAGGcCAAATGTTCACTTA
CCGC - cTATACGTCCGgGACcGTGCggggCAGTGTtTcTGGTAGGcCAaATGTTCAcCTTA

SEO ID NO: Isolate

45 SA1
47 SA5
49 SA7
46 SA4
50 SA13
48 SA6
45-50 consensus

306 TAGGCCTCGCCAGCATAcAcAGTGAGGACTGCAACTGTTCCATTtTACAGtGGCCATATC
306 TAGGCCTCGCCAGCATAcTACGGTGcAGGACTGCAACTGTTCCATTtTACAGcGGCCATATC
306 TAGGCCTCGCCAGCACAcTACGGTGcAGGACTGCAACTGTTCCATTtTACAGtGGCCATATC
306 TAGGCCTCGCCAGCACAcTACGGTGcAaGACTGCAAtTgCTcATTtTACAGtGGCCATATC
306 TAGcCCTGCcCGCATaATgTtGTGcAGGACTGCAACTGtTCCATTtTACAGtGGCCaATC
306 TAGgCCTCGCCaGcATgCTacgGTaCAGGACTGCAACTGcTCCATTtTACAGtGGCCaATC
TAGgCCTCGCCaGcATaactacgGTgCagGACTGCAACTGtTcCAATTtTACAGtGGCCaATC

SEO ID NO: Isolate

45 SA1
47 SA5
49 SA7
46 SA4
50 SA13
48 SA6
45-50 consensus

367 ACCGGCCACCGgATGGCtTGGGACATGATGATGAATTGGTCACCTACGACAGCCTTgGTGA
367 ACCGGCCACCGAATGGcATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTgGTGA
367 ACCGGCCACCGAATGGcATGGGACATGATGATGAATTGGTCACCTACGACAGCCTTgGTGA
367 ACCGGCCACCGGATGGcATGGGACATGATGATGAATTGGTCACCTACGACgCCTTgGTGA
367 ACCGGCCACCGGATGGcATGGGACATGATGATGAATTGGTCACCTACaACAGcCTTgGTGA
367 ACtGGCCACCGGATGGcATGGGACATGATGATGAATTGGTCACCgCgACAGcCTTgGTGA
ACcGGCCACCGgATGGcATGGGACATGATGATGAATTGGTCACCTaCgACAGcCTTgGTGA

FIGURE 1G

SEQ ID NO: Isolate

45 SA1

47 SA5

49 SA7

46 SA4

50 SA13

48 SA6

45-50 consensus

428 TGGCCCAgATGCTACGGATcCCCCAgGTGGTCATaGACATCATaGCCGGGGGCCACTGGGG
 428 TGGCCCAgGTGCTACGGATTCCCCAaGTGGTCATtGACATCATtGCCGGGGGCCACTGGGG
 428 TGGCCCAgTTGCTACGGATTCCCCAGGTGGTCATCGACATCATtGCCGGGGGCCACTGGGG
 428 TGGCCCAgTTGCTACGGATTCCCCAGGTGGTCATCGACATCATtGCCGGGGGCCACTGGGG
 428 TGGCCCAgTTGCTACGGATTCCCCAGGTGGTCATTGACATCATtGCCGGGGGCCACTGGGG
 428 TGGCCCAaaTGcTACGGATTCCCCAGGTGGTCATTGACATCATtGCCGGGGGCCACTGGGG
 TGGCCCAgTtTGcTACGGATtCCCCAgGTGGTCATtGACATCATtGCCGGGGGCCACTGGGG

SEQ ID NO: Isolate

45 SA1

47 SA5

49 SA7

46 SA4

50 SA13

48 SA6

45-50 consensus

489 GGTCTTGTTtGCCGcCGCATACTTtCGCTGcGCcGCcAACTGGGCTAAGGTaGTGCTGGTt
 489 GGTCTTGTTtCGCCGtCGCATACTtCGCGTCAGCGGCTAACTGGGCTAAGGTTGTGCTGGTC
 489 GGTCTTGTTtCGCCGCGCGCATATtTCGCGTCAGCGGCTAACTGGGCTAAGGTTGTGCTGGTC
 489 GGTCTTGTTtGCCGCGCGCATATtTCGCGTCAGCGGCTAACTGGGCTAAGGTTaTaCTGGTC
 489 GGTCTTGTTtCGCCGCGCGCATActaCGCGTCGCGGGCTAACTGGGCTAAGGTTGTGCTGGTC
 489 GGTCTTGTTtCGCCGCGCGCATACTtCGCGTCGCGGGCTAACTGGGCTAAGGTTGTGCTGGTC
 GGTCTTGTTtGCCGcCGCATActtCGCGTC - GCgGCTAACTGGGCTAAGGTtGTgCTGGTc

SEQ ID NO: Isolate

45 SA1

47 SA5

49 SA7

46 SA4

50 SA13

48 SA6

45-50 consensus

550 CTGTTtCTGTTtGCGGGGGTCGATGGC
 550 CTGTTtCTGTTtGCGGGGGTCGATGGC
 550 TGTTTtCTGTTtGCGGGGGTCGATGCC
 550 TGTTTtCTGTTtGCGGGGGTCGATGCC
 550 CTGTTtCTGTTtGCGGGGGTCGATGCC
 550 tTGTTtCTGTTtGCGGGGGTCGATGCC
 -TGTTtCTGTTtGCGGGGGTCGATGCC

[illegible]

1-51 consensus

T A T T CA CC GG TG T CC TG C

123 CAATGGCCACCCTCGCTGCTGGTATACAAGTgACACTTAATGTGGCTGTGAACACCGCGCGC
124 CGCCACAGCTCTTCGATGTGGTGGTCGGGTGACCCCAATCTCGCCATCAAGTCAACCTGGC
125 GCGAAATaCaTtCCgGTGCTGGTATACCGGTCTcCGCAATGTCGCGGTGCaGCaCGCGCGG
126 CGGCAATACATGcACGTGTGGACCCcACGTAGACATcTCAAGTGTGCGGTGCaGCaCGCGCGG
127 gaaCaCcttCtTCcGcGTGTGGGTgAGCGTcTcACcAGCTGTGGCAGTTCAGGTAGCTCGGA
128 GTGgTaaCgcctCGAGTGTGGTGTGGTGTgTGAaCCCCACcGTGTGGCAGTgAGGcCGAG
129 TGGGAACATACCTCGGTTGTCTGGACGCGCGGTGACCGTCAcAGTGGCTGTGCGACACCGCGG
130 TGGGAATcCAGTCACTGCTGGGTGGCGCTTAACTCCACcGTGGCGGTgTCTTATATCGAT
131 AGGGAACAAGTCTACATCTCGGGTGTCTCTcACCCcACCGGTGGTCGCGCAACATCTGGAAT
132 GGAGAATACCTCTCGCTCGTGGGTGCCTTTACACCCCACTGTGGCGCGCGCTATCCGAAT
133 agATATGTTCAGTAgTGTCTGGGTcCAaATCACCCCAcATgTTCAGCAGCGGAacCTCGGA
134 CGGTAAGTCGGTGTCACTGTGGCATGTGTGACACCCCACTGTGCGATACCAATGTTCTG

TG TGG T C C C A T C

24892

FIGURE 1H

SEO ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

428 TcGCCTAtGcGcTcCGTGTtCCTGAgCTAGtCCTtgAaGtTGTCTTCGGcGGcCATTGGGG
 428 TGGCGTACTTGGTGGCATCCCGGAAGTCATCTTGACATATTGTTACAGGAGGTCATTGGGG
 428 TGGCGTACGcGATGCGCGTTCGCCAGGTCATCTAGACATCaTtagCGGgGCTcACtTGGGG
 428 TgGCGCAGcTcTGGCgttTGCCcAGACctTGTTtGACATaATagCcGGGGCCCACTGGGG
 428 TaTCGCAgtTaTCCCGgaTCCCaCAAGCTgTcGTGGaCaTGGTggCgGGgGCCACTGGGG
 428 TaGctCAGCTGCTCcGgaTCCCGCaAGCcaTCTTGGaCaATGATCGCTGGtGcCaCTGGGG
 428 TCGCCcAGATCATGAGGGTCCCCCAAGCCTTTCTCGACATGGTTCGCCGAGGCCACTGGGG
 428 TCGCCcAGGTcATGAGGATCCCTAGCACTCTGGTAgATCTACTGcCTGAGAGGCCACTGGGG
 428 TCGCCCAACTtATGAGGATCCcAGGCGCCATGGTTCGACCTGCTTCcAGGCGCGCTACTGGGG
 428 TGGCTCAGATCTTACGGATCCCTCTATCTAGGTGACTTGGCTCAcCGGGgCTACTGGGG
 428 TGGCCCAgtTGcTACGGATtCCCCagGTGGTCATtGACATCAAtGCCGGGgGCCACTGGGG
 428 TATCTAGCATCTTgAGGGTACCTGAGATTTGTGCGAGTGTGATATTGTGGTCCATTGGGG

T C G T CC T T GG G CA TGGGG

SEO ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

489 cGTGGTgTTTGGCTTGGCCtATTtTCCATGcAGGGAGCGTGGGCCAAAGTCATtGCCATC
 489 TGTAATGTTTGGCCTCGCTTACTTCTCCATGcAGGGATCGTGGGGCAAGGTCATCGTTATC
 489 CGTCaTGTtTcGGctTaGcCTACTTCTCTATGcAGGGAGCGTGGGCCAAAGTCgTTGTATC
 489 CATCtTGGCgGGCCTAGCCtATTaCTcATGcAGGGCAACTGGGCCAAAGTTCGTATCaATC
 489 agTCTTgCGGGCCtTGCcTACTaTCCATGGtGGGgAACTGGGCTAAAGTtTgATTGTg
 489 AGTCTcAGCGGCGATAGCGTATTtTCCATGGtGGGgAACTGGGCGAAAGTtTgATTGTg
 489 CGTCTCCGCGGCGTTGGCGTACTTcAGCATGcAAGGCAATTGGGCCAAAGTtAGTCTGGTTC
 489 cgTCTTgTtGGGtTGGCgTACTTcAGCATGcAAGGCAATTGGGCCAAAGTtATcCTGGTTC
 489 CATTCCTGGTTGGCATAGCGTACTTcAGCATGcAAGGCAATTGGGCCAAAGTtATCCTGGTTC
 489 AGTTCCTGGTCTAGCTTCTTcAGCATGcAAGGCAATTGGGCCAAAGTtATCCTGGTTC
 489 GGTCTCTGTTcGCCGccGATAcTtCGCGTCgGCGcTAACTGGGCTAAAGTtGTgCTGGTc
 489 GATACTACTAGCCGTTCCTACTTtTGGCATGGCTGGCAACTGGCTAAAAGTtTCTGGCTGTT

T T G GC T T TGG AA GT T

SEO ID NO: Genotype

30-33 (IV/2b)
 34 (2c)
 26-29 (III/2a)
 35-39 (V/3a)
 9-25 (II/1b)
 1-8 (I/1a)
 40 (4a)
 42-43 (4c)
 44 (4d)
 41 (4b)
 45-50 (5a)
 51 (6a)

1-51 consensus

550 CTCCTtCTGTcGcAGGAGTGGATGCA
 550 CTCCTGCTGACTGCTGGGGTGGAGCGG
 550 CTtTGTCTggCcGCTGGGgTCCGATGCC
 550 ATGgTTATGTtTTcAGGgTCCGATGCC
 550 aTGTACTctTTGcCGGcGTtGAcGGg
 550 CTGtTGTCTgtTtGcCGGCGTcGATGCG
 550 CTTTTCCTCTTTGCTGGGGTAgAGGCC
 550 CTTTTCCTCTCTcGTGAGGTTGATGCC
 550 CTGTTTCTCTTGTCTGGAGTTCGACGCT
 550 CTATTCTCTTTGGCGGGGTcGAGGGA
 550 tTGTtTCTGTTTGGGGGGTcGATGcC
 550 CTGTTCTATTtGcAGGGTtGAAGCA

T T T C GG GT GA G

FIGURE 2A

<u>SEQ ID NO:</u>	<u>Isolate</u>	
56	S14	184 LLLFAGVDA
52	DK7	184 LLLFAGVDA
59	US11	184 LLLFAGVDA
55	DR4	184 LLLFAGVDA
54	DR1	184 LLLFAGVDA
53	DK9	184 LLLFtGVDA
58	SW1	184 LLLFtGVDA
57	S18	184 LLLFaGVDA
52-59	consensus	LLLFaGVDA

FIGURE 2B

SEQ ID NO:	Isolate	
75	T10	1 YEVRNVSGmYHVTNDCSNSSIVFEAdlIMHTPGCVPVRegNsSRCWVALTPTLAARntS
62	DK1	1 YEVRNVSGvYHVTNDCSNSSIVFEAvDvIMHTPGCVPVRENhSRCWVALTPTLAARNAS
64	HK4	1 hEVhNVSGiYHVTNDCSNSSIVFEADMIHMTPGCVPVRENSSRCWVALTPTLAARNAS
76	US6	1 YEVRNVSGmYHVTNDCSNSSIVFEADMIHMTPGCVPVRENSSRCWVALTPTLAARNAS
68	IND8	1 YEVRNVSGvYHVTNDCSNSSIVFEADMIHMTPGCVPVREGNfSeCWVALTPTLAARNAS
67	IND5	1 YEVRNVSGvYHVTNDCSNSSIVFEADMIHMTPGCVPVREGNSSRCWVALTPTLAARNAS
73	SW2	1 YEVRNVSGvYHVTNDCSNSSIVYETADMIHMTPGCVPVREaNSRCWVALTPTLAARntS
63	HK3	1 YEVRNVSGiYHVTNDCSNSSvVYETADMIHMTPGCVPVRENSSRCWVALTPTLAARNVS
66	HK8	1 YEVRNVSGiYHVTNDCSNSSIVYETADMIHMTPGCmPCVRENSSRCWVALTPTLAARNVS
61	D3	1 YEVRNVSGVYqVTNDCSNSSIVYETADMIHMTPGCVPVREdNSSRCWVALTPTLAARNsS
74	T3	1 YEVRNVSGVYyVTNDCSNSSIVYETADMIHMTPGCVPVREsNSSRCWVALTPTLAARNAS
65	HK5	1 YEVRNVSGvYHVTNDCSNlSIVYETdMIHMTPGCVPVRENSSRCWVALaPTLAARNAS
71	S45	1 YEVRNVSGaYHVTNDCSNSSIVFEAvDvIiHTPGCVPVRENSSRCWVALTPTLAARNSS
72	SA10	1 YEVRNVSGmYHVTNDCSNSSIVFEADMIHMTPGCVPVRENSSRCWVALTPTLAARNSS
69	P10	1 YEVRNVSGvYHVTNDCSNSSIVFEADMIHMTPGCVPVRENSSRCWVALTPTLAARNSS
60	D1	1 YEVRNVSGvYHVTNDCSNSSIVYELADMIHMTPGCVPVREdNSSRCWVALTPTLAARNgn
70	S9	1 YEVRNVSGaYHVTNDCSNSSIVFEADvIMHTPGCVPVqEgNSSqCWVALTPTLAARNat
60-76	consensus	yEVrNVSGvYhVTNDCSNsSiVyEaaDmImHTPGCvPCVrEnNsSrCWVALtPTLAARNas

FIGURE 2B

SEQ ID NO:	Isolate	
75	T10	62 vPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETIQDCNCISIYPGH1
62	DK1	62 IPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETaQDCNCISIYPGHV
64	HK4	62 IPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
76	US6	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLiSQLFTFSPrqHETVQDCNCISIYPGHV
68	IND8	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
67	IND5	62 VsTTTIRrhVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
73	SW2	62 VPTTTIRRHVDLLVGAAAFCSvMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
63	HK3	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
66	HK8	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
61	D3	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQeCNCISIYPGHV
74	T3	62 VPTKtIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
65	HK5	62 VPTTaIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
71	S45	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRHETVQDCNCISIYPGHV
72	SA10	62 VPTTTIRRHVDLLVGAAAFCSAMYVGDLCGSVFLVSQLFTFSPPRRyETVQDCNCISIYPGrV
69	P10	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSVLLVSQLFTFSPPRRhTVQDCNCISIYPGHV
60	D1	62 VPTTAIRRHVDLLVGAAAFCSAMYVGDLCGSVFLiSQLFTiSPRRHETVQeCNCISIYPGHV
70	S9	62 VPTTtIRRHVDLLVGAAAFCSAMYVGDLCGSVFLiSQLFTiSPRRHETVQnCNCISIYPGHV
60-76	consensus	vpTttIRrhVDLLVGAAAFCSaMYVGDLCGSVFLvSQLFTFSPPRRheTvQdCNCISIYPGHv

FIGURE 2B

SEQ ID NO:	Isolate	
75	T10	123 SGHRMAWDMMNWSPPTALVVSQLLRIPQAVMDMvtGAHWGVLAGLAYYSMAGNWAKVLI
62	DK1	123 SGHRMAWDMMNWSPPTALV1SQLLRIPQAVVDMVAGAHWGVLAGLAYYSMAGNWAKVLI
64	HK4	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
76	US6	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
68	IND8	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLI
67	IND5	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGILAGLAYYSMVGNWAKVLI
73	SW2	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
63	HK3	123 SGHRMAWDMMNWSPTAALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
66	HK8	123 SGHRMAWDMMNWSPtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLI
61	D3	123 TGHRMAWDMMNWSPtALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
74	T3	123 TGHRMAWDMMNWSPtTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
65	HK5	123 TGHRMAWDMMNWSPtTALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
71	S45	123 TGHRMAWDMMNWSPtALVVSQLLRIPQAVVDMVAGAHWGVLAGLAYYSMVGNWAKVLI
72	SA10	123 TGHRMAWDMMNWSPtALVVSQLLRIPQAIvDMVAGAHWGVLAGLAYYSMVGNWAKVLI
69	P10	123 sGHRMAWDMMNWSPtALVVSQLLRIPQAI1DvVAGAHWGVLAGLAYYSMVGNWAKVLI
60	D1	123 TGHRMAWDMMNWSPtTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
70	S9	123 TGHRMAWDMMNWSPtTALVVSQLLRIPQAVMDMVAGAHWGVLAGLAYYSMVGNWAKVLI
60-76	consensus	sGHRMAWDMMNWSPtALVVSQLLRiPQAvvDmVaGAHWGVLAGLAYYSMvGNWAKVLI

FIGURE 2B

<u>SEQ ID NO:</u>	<u>Isolate</u>	
75	T10	184 mLLFAGVDG
62	DK1	184 lLLFAGVDG
64	HK4	184 mLLFAGVDG
76	US6	184 lLLFAGVDG
68	IND8	184 MLLFAGVDG
67	IND5	184 MLLFAGVDG
73	SW2	184 MLLFAGVDG
63	HK3	184 MLLFAGVDG
66	HK8	184 MLLFAGVDG
61	D3	184 MLLFAGVDG
74	T3	184 lLLFAGVDG
65	HK5	184 MLLFAGVDG
71	S45	184 MLLFAGVDG
72	SA10	184 MLLFAGVDG
69	P10	184 MLLFAGVDG
60	D1	184 MLLFAGVDG
70	S9	184 MLLFAGVDG
60-76	consensus	mLLFAGVDG

FIGURE 2C

<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	1 A QVrNTsrgYmVTNDCSNeSITWQLQAAVLHVPGCIPCRlGNTSRCWIPVtPNVAVRQPG
78	T4	1 A QVKNTttnSYmVTNDCSNDsITWQLQAAVLHVPGCVPCekGNTSRCWIPVSPNVAVRQPG
79	T9	1 AeVKNTSTSYmVTNDCSNDsITWQLQAAVLHVPGCVPCERVGNaSRCWIPVSPNVAVRQPG
80	US10	1 vqVKNTSTSYmVTNDCSNDsITWQLQAAVLHVPGCVPCekVGNTSRCWIPVSPNVAVRQPG
77-80	consensus	aqVKnTsttsYmVTNDCSNDsITWQLQAAVLHVPGCVPCe-vGNTSRCWIPVsPNVAV--PG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMMLAAQMFIVSPrrHWFVQeCNCsIYPGTI
78	T4	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMMLAAQMFIVSPQHWFVQdCNCsIYPGTI
79	T9	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMMLAAQMFIIiSPQHWFVQeCNCsIYPGTI
80	US10	62 ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMMLAAQMFIVSPrHhFVQeCNCsIYPGTI
77-80	consensus	ALTQGLRTHIDMVMSATLCSALYVGDLCCGVMMLAAQMFIVSP-hHwFVQeCNCsIYPGTI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	123 TGHrMAWdMMNWSPTATmILAYAMRVPEVIIdIiGGAHwGVmFGLAYFSMQGAWAKVVI
78	T4	123 TGHrMAWdMMNWSPTATmILAYAMRVPEVIIdIVsGAHwGVmFGLAYFSMQGAWAKVVVI
79	T9	123 TGHrMAWdMMNWSPTtTmILAYAMRVPEVIIdIISGAHwGVmFGLAYFSMQGAWAKVVVI
80	US10	123 TGHrMAWdMMNWSPTaTlILAYAMRVPEVIIdIISGAHwGVlFGLAYFSMQGAWAKVVVI
77-80	consensus	TGHrMAWdMMNWSPTaTmILAYAMRVPEVIIdIISGAHwGVmFGLAYFSMQGAWAKV-VVI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
77	T2	164 LLLAAGVDA
78	T4	164 LLLAAGVDA
79	T9	164 LLLtAGVDA
80	US10	164 LLLaAGVDA
77-80	consensus	LLLaAGVDA

FIGURE 2D

SEQ ID NO:	Isolate	
82	DK11	1 VEVRRNTSSSYATNDCSNNSITWQLTNAVHLHLPVCPCENDNGTLHCWIQVTPNVAVKHRG
83	SW3	1 VEVRRNISSSYYATNDCSNNSITWQLTNAVHLHLPVCPCENDNGTLHCWIQVTPNVAVKHRG
84	T8	1 VEVRRNTSfSSYYATNDCSNNSITWQLTNAVHLHLPVCPCENDNGTLRCWIQVTPNVAVKHRG
81	DK8	1 VEVRRNISsSSYYATNDCSNNSITWQLTNAVHLHLPVCPCENDNGTLRCWIQVTPNVAVKHRG
81-84	consensus	VEVRRN-SsSSYYATNDCSNNSITWQLTNAVHLHLPVCPCENDNGTL-CWIQVTPNVAVKHRG

SEQ ID NO:	Isolate	
82	DK11	62 ALTHNLRRAHIDMIVMAATVCSALYVGDvCGAVMIVSQAFIvSPehHhFTQECNCsIYQGHl
83	SW3	62 ALTHNLRRAHVDMIVMAATVCSALYVGDmCGAVMIVSQAFIISPERHNFTQECNCsIYQGRI
84	T8	62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIaSQAFIISPERHNFTQECNCsIYQGHl
81	DK8	62 ALTHNLRTHVDVIVMAATVCSALYVGDVCGAVMIvSQALIIISPERHNFTQECNCsIYQGHl
81-84	consensus	ALTHNLR-HvD-IVMAATVCSALYVGDvCGAVMIvSQAFIISPERHhFTQECNCsIYQGHl

SEQ ID NO:	Isolate	
82	DK11	123 TGHRAWDMDMLNWSPTLTMLAYAAARVPELVLEVVFGGHWGVVFLAYFSMQGAWAKVIAI
83	SW3	123 TGHRAWDMDMLNWSPTLTMLAYAAARVPELVLEVVFGGHWGVVFLAYFSMQGAWAKVIAI
84	T8	123 TGHRAWDMDMLNWSPTLTMLAYAAARVPELVLEVVFGGHWGVVFLAYFSMQGAWAKVIAI
81	DK8	123 TGHRAWDMDMLNWSPTLTMLAYAAARVPELaLqVVVFGGHWGVVFLAYFSMQGAWAKVIAI
81-84	consensus	TGHRAWDMDMLNWSPTLTMLAYAAARVPELVLeVVVFGGHWGVVFLAYFSMQGAWAKVIAI

SEQ ID NO:	Isolate	
82	DK11	184 LLLVAGVDA
83	SW3	184 LLLVAGVDA
84	T8	184 LLLVAGVDA
81	DK8	184 LLLVAGVDA
81-84	consensus	LLLAVGVDA

FIGURE 2E

<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	1 LEWRNVSGLYVLTNDCsNSSIIVYEADDVILHTPGCVPCVQDGNSTCWTSVTPTVAVRYVG
87	HK10	1 LEWRNVSGLYVLTNDCpNSSIIVYEADDVILHTPGCVPCVQDGNSTCWTSVTPTVAVRYVG
88	S2	1 LEWRNTSGLYVLTNDCSNSSIIVYEADDVILHTPGCVPCVQDGNSTCWTSPVTPTVAVRYVG
90	S54	1 LEWRNTSGLYiLTNDCSNSSIIVYEADDVILHTPGCVPCVQDGNSTCWTSPVTPTVAVRYVG
89	S52	1 LEWRNTSGLYvLTNDCSNSSIIVYEADDVILHTPGCVPCVQDGNSTmCWTSPVTPTVAVRYVG
86-90	consensus	LEWRNTSGLYvLTNDCsNSSIIVYEADDVILHTPGCVPCVQDGNSTcCWTpVTPTVAVRYVG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	62 ATTASIRSHVDLLVGAAATMCSALYVGdVCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
87	HK10	62 ATTASIRSHVDLLVGAAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
88	S2	62 ATTASIRSHVDLLVGAAATMCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
90	S54	62 ATTASIRSHVDLLVGAAATLCALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
89	S52	62 ATTASIRSHVDLLVGAAATLCALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHV
86-90	consensus	ATTASIRSHVDLLVGAAATmCSALYVGDMCGAVFLVGQAFTFRPRRHQTVQTCNCSLYPGHL
<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	123 SGHRMAWDMmNWSPAVGMVVAHVLRPLQTLFDIIAGAHWGImAGLAYYSMOGNWAKVAII
87	HK10	123 SGHRMAWDMmNWSPAVGMVVAHVLRPLQTLFDIIAGAHWGILAGLAYYSMOGNWAKVAII
88	S2	123 SGHRMAWDMmNWSPAVGMVVAHVLRPLQTVFDIIAGAHWGILAGLAYYSMOGNWAKVAII
90	S54	123 SGHRMAWDMmNWSPAVGMVVAHILRPLQTLFDILAGAHWGILAGLAYYSMOGNWAKVAII
89	S52	123 SGHRMAWDMmNWSPAVGMVVAHILRPLQTLFDILAGAHWGILAGLAYYSMOGNWAKVAIv
86-90	consensus	SGHRMAWDMmNWSPAVGMVVAHVLRPLQTLFDIIAGAHWGILAGLAYYSMOGNWAKVAII
<u>SEQ ID NO:</u>	<u>Isolate</u>	
86	DK12	184 MVMFSGVDA
87	HK10	184 MVMFSGVDA
88	S2	184 MVMFSGVDA
90	S54	184 MIMFSGVDA
89	S52	184 MIMFSGVDA
86-90	consensus	MVMFSGVDA

[illegible]

93-94 consensus (Z6)

1 VNYhNASGVYHtNDPCNSSImYEAHHILHLPGLPCVrGNGQSRCWALTPTVAAPYIG
1 VNYrNASGVYHVNDPCNSSiVYEAHqILHLPGLPCVrGNGQSRCWALTPTVAvsYIG
VNYrNASGVYHVNDPCNSSiVYEAHqILHLPGLPCVrGNGQSRCWALTPTVAvsYIG

93-94 consensus (Z6)

62 APLESIRRHVDLMVGAATVCSALYIGDLCCGGVFLVGOMFSFQPRRHWTQDCNCISIYAGHV
62 APLdSLRRHVDLMVGAATVCSALYgDLCGGaFLVGOMFSFQPRRHWTQDCNCISIYAGHi
APLdSLRRHVDLMVGAATVCSALYgDLCGGaFLVGOMFSFQPRRHWTQDCNCISIYAGHi

93-94 consensus (Z6)

123 TGHRMAWDDMMNNWSPTTTLVLAQVMRI PSTLVDLLTGGHWGILiGvAYFCMQANWAKVILV
123 TGHRMAWDDMMNNWSPTTTLVLAQVMRI PSTLVDLLAGGHWGvLVGLIAYFSMQANWAKVILV
TGHRMAWDDMMNNWSPTTTLVLAQVMRI PSTLVDLLAGGHWGvLVGLIAYFCMQANWAKVILV

93-94 consensus (26)

```

184 LFLyAGVDA
    ||| ||||
184 LFLFAGVDA
    LFLfAGVDA

```


FIGURE 2G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	1 VPYRNASGVYHVTNDPCNSSIYVEADNLILHAPGCVPCVkegNVSRCWQITPTLSAPNLG
100	SA7	1 VPYRNASGVYHVTNDPCNSSIYVEADNLILHAPGCVPCVRQnNVSRCWQITPTLSAPNLG
97	SA4	1 VPYRNASGVYHVTNDPCNSSIYVEADNLILHAPGCVPCVRQDNVSkCWQITPTLSAPNLG
96	SA1	1 VPYRNASGVYHVTNDPCNSSIYVEADsLILHAPGCVPCVRQDNVSRCWQITPTLSAPtfg
99	SA6	1 VPYRNASGVYHVTNDPCNSSIYVEADDLILHAPGCVPCVRkdNVSRCWvhitPTLSAPSLG
101	SA13	1 VPYRNASGVYHVTNDPCNSSIYVEADDLILHAPGCVPCVRqgNVSRCWqITPTLSAPSLG
96-101	consensus	VPYRNASGVYHVTNDPCNSSIYVEADnLILHAPGCVPCVrqdNVsrCWvqITPTLSAPnLG
<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	62 AVTAPLRRvVDYLAGGAALCSALYVGDACGAVFLVGQMFtYrPRQHTTVQDCNCsIYSGHI
100	SA7	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFsYrPRQHTTVQDCNCsIYSGHI
97	SA4	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFTYrPRQHTTVQDCNCsIYSGHI
96	SA1	62 AVTAPLRRAVDYLAGGAALCSALYVGDACGAVFLVGQMFtYrPRQHTTVQDCNCsIYSGHI
99	SA6	62 AVTAPLRRAVDYLAGGAALCSALYVGdVCGAlFLVGQMFTYrPRQHatVQDCNCsIYSGHI
101	SA13	62 AVTAPLRRAVDYLAGGAALCSALYVGDaCGAvFLVGQMFTsPrRhnvQDCNCsIYSGHI
96-101	consensus	AVTAPLRRaVDYLAGGAALCSALYVGDaCGAvFLVGQMFtYrPrQHttVQDCNCsIYSGHI
<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	123 TGHrMAWdMMMNwSPtTAlvMAQvLRIpQVVIdIIAGGHwGVLFAvAYFASAANwAKVVLv
100	SA7	123 TGHrMAWdMMMNwSPtTAlvMAQLLRIpQVVIdIIAGGHwGVLFAAAyFASAANwAKVVLv
97	SA4	123 TGHrMAWdMMMNwSPtTAlvMAQLLRIpQVVIdIIAGGHwGVLFAAAyFASAANwAKVVLv
96	SA1	123 TGHrMAWdMMMNwSPtTAlvMAQMLRIpQVVIdIIAGGHwGVLFAAAyFASAANwAKVVLv
99	SA6	123 TGHrMAWdMMMNwSPaTAlvMAQMLRIpQVVIdIIAGGHwGVLFAAAyFASAANwAKVVLv
101	SA13	123 TGHrMAWdMMMNwSPtAlvMAQLLRIpQVVIdIIAGaHwGVLFAAAyFASAANwAKVVLv
96-101	consensus	TGHrMAWdMMMNwSPtAlvMAQLLRIpQVVIdIIAGGHwGVLFAaAYFASAANwAKVVLv

FIGURE 2G

<u>SEQ ID NO:</u>	<u>Isolate</u>	
98	SA5	184 LFLFAGVDg
100	SA7	184 LFLFAGVDA
97	SA4	184 LFLFAGVDA
96	SA1	184 LFLFAGVDg
99	SA6	184 LFLFAGVDA
101	SA13	184 LFLFAGVDA
96-101	consensus	LFLFAGVDA

1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0
 1000
 900
 800
 700
 600
 500
 400
 300
 200
 100
 0

FIGURE 2H

SEQ ID NO: Genotype

81-84 (IV/2b)
 85 (2c)
 77-80 (III/2a)
 86-90 (V/3a)
 60-76 (II/1b)
 52-59 (I/1a)
 91 (4a)
 93-94 (4c)
 95 (4d)
 92 (4b)
 96-101 (5a)
 102 (6a)

52-102 consensus

1 VEVNRNisSYYATNDCSNnSITWQLTnAVLHLPgcVPCENDNGTLrCWIQVTPNVAVKHRC
 1 VEVKDTGDSYMPNTNDCSNSSIVWQLGAVLHTPGCVPCERTANVSRCWVPVAPNLAIISQPC
 1 aqVktstSYMTNDCSNdSITWQLGAALVHPGCVPCExvGNTSRcWIPVSPNVAIVqGPC
 1 LEWRNtSGLYvLTNDCnSSIVYEADDVILHTPGCVPCVQDNGTSctCWtpVTPTVAARYVC
 1 yEVrNVSGvYhVTNDCSNsSiVyEaAdImHTPGCVPCVrEnNsSrCWALtPTLAARNAs
 1 yQVRNstGLYHVTNDCPNSSIVYEaADaILHsPGCVPCVREgnasrCWAvtPTVATRDGH
 1 EHYRNASGIYHITNDCPNSSIVYEADHILHLPGCVPCVMTGNTSRcWTPVTPTVAVAHPC
 1 VNYrNASGVYHvTNDcPNSSivYEAHQILHLPGCLPCVrvGNQSRcWALtPTVAvsYIC
 1 YNVRNssGVYHVTNDCPNSSIVYETTYHILHLPGCVPCVREGNKSTcWsvLTPtVAAQHLL
 1 VHYRNASGVYHVTNDCPNSTIVYETHEHIMHLPGCVPCVRENTSRcWVPLTPTLAAPYPh
 1 VPYRNASGVYHVTNDCPNSSIVYEADnLILHAPGCVPCVrQdNVsrCWVqITPTLASAPnLC
 1 LTYGNSSGLYHLTNDcPNSSIVLEADAMILHLPGCLPCVRVDDRSCTCWAHvTPTLAIPNAS

Y TND C N S H PGC PC CW H P

SEQ ID NO: Genotype

81-84 (IV/2b)
 85 (2c)
 77-80 (III/2a)
 86-90 (V/3a)
 60-76 (II/1b)
 52-59 (I/1a)
 91 (4a)
 93-94 (4c)
 95 (4d)
 92 (4b)
 96-101 (5a)
 102 (6a)

52-102 consensus

62 ALTHNLRtHvDmIVMAATVCSALYVGdVCGAVMIvSQAFiISPERHnFTQECNCSiYQGHl
 62 ALTKGLRAHIDIIVMSATVCSALYVGdVCGALMLAAQVVVVSPQHHTFVQECNCSiYPGRl
 62 ALTQGLRTHIDMVMSATLCSALYVGdLCGGvMLAAQMFIVSpqhHvFVQeCNCsiYPGTI
 62 ATTASIRSHVDLLVGAATmCSALYVGdMCGAVFLVGQAFtFPRRRHQTVQTCNCSLYPGHl
 62 vpTttIRrHVDLLVGAaFCSaMYVGdLcGSVfLVsQLFTfSPRRheTvQdCNCsiYPGHv
 62 LPatQLRRhIDLLVGSATLCSALYVGdLcGSVfLVsQLFTfSPRRheWTTQdCNCsiYPGHl
 62 APLESFRHHVDLMVGAATLCSALYVGdLcGGAFLMGQMTfPRRRHWTTQECNCSiYTGHI
 62 APLdsIRHHVDLMVGAATVCSALYVGdLcGGAFVLVGQMFSPQPRRHWTQdCNCsiYAGHI
 62 APLESIRHHVDLMVGAATLCSALYVGdLcGGVFLVGQLFTfQPRRHWTQdCNCsiYTGHI
 62 APLESIRHHVDLMVGAATMCSAFYIGdLcGGVFLVGQLFDFPRRRHWTTQdCNCsiYPGHl
 62 AVTAPLIRaVDYLAGGALCSALYVGdaCGAVFLVGQMFtYPRqHttVQdCNCsiYSGHI
 62 TPATGFRHHVDLLAGAAVVCSSLYIGdLcGSFLAGQLFTfQPRRHWTQdCNCsiYTGHI

R D A CS Y GD CG Q P Q CNCs Y G

SEQ ID NO: Genotype

81-84 (IV/2b)
 85 (2c)
 77-80 (III/2a)
 86-90 (V/3a)
 60-76 (II/1b)
 52-59 (I/1a)
 91 (4a)
 93-94 (4c)
 95 (4d)
 92 (4b)
 96-101 (5a)
 102 (6a)

52-102 consensus

123 TGHRMAWdMMNWSPTTLTMLAYAAARVPeLVLeVVFGGHWGVVFLGAYFSMQGAWAKVIAI
 123 TGHRMAWdMMNWSPTTTLMLAYLVRIPEVILDIvTGGHWGVVFLGAYFSMQGSWAKVIVI
 123 TGHRMAWdMMNWSPTaTmILAYaMRVPEVIdiIsaHGWGVVFLGAYFSMQGAWAKVIVI
 123 SGHRMAWdMMNWSPAVGMVVAHVLRLPQTIFDIAGAHWGILLAGLAYSMSQGNWAKVIAI
 123 sGHRMAWdMMNWSPTaALVVSQLLRIPOAvDmVGAHGWGVLAGLAYSMSQGNWAKVILV
 123 TGHRMAWdMMNWSPTtALVvQALLRIPOAIdLMIAGAHWGVLGAGIAYFSMvGNWAKVIVV
 123 TGHRMAWdMMNWSPTTTLILAQIMRVPTAFLDmVAGHGWGVLAGLAYSMSQGNWAKVILV
 123 TGHRMAWdMMNWSPTTTLILAQVMRIPSTLVdLLaGHHWGVVGLAYFSMQGNWAKVILV
 123 TGHRMAWdMMNWSPTATLVLAQIMRIPGAMVDLLAGHGWGLVGTAYFSMQGNWAKVILV
 123 SGHRMAWdMMNWSPTSALIMAQILRIPSIIGDLLTGGHGWGVLAGLAFFSMQGNWAKVILV
 123 TGHRMAWdMMNWSPTALvMAQILRIPQVVIDIAGHGWGVLFaaYfASAAANWAKVILV
 123 TGHRMAWdMMNWSPTTTLVSSILRVPEICASVIFGGHGWGILLAVAYFGMAGNWLKVLAV

GHRMAWdMM NWSP R P G HWG A W KV

FIGURE 2H

<u>SEQ ID NO:</u>	<u>Genotype</u>		
81-84	(IV/2b)	184	LLL V AGVDA
85	(2c)	184	LLL T AGVEA
77-80	(III/2a)	184	LLL a AGVDA
86-90	(V/3a)	184	MvMFSGVDA
60-76	(II/1b)	184	mLLFAGVDG
52-59	(I/1a)	184	LLL F aGVDA
91	(4a)	184	LFLFAGVDA
93-94	(4c)	184	LFL f AGVDA
95	(4d)	184	LFLFAGVDA
92	(4b)	184	LFLFAGVEG
96-101	(5a)	184	LFLFAGVda
102	(6a)	184	LFLFAGVEA
52-102	consensus		GV

FIGURE 3

Genotype	SEQ ID NO:	Isolate	gQ1ffaprrhwt-cOdnc5n1pghitGHRMAMWNSpLcaqvq1R1Pcav1dmvcaHwGv1ag1yfvsmvgnWkV1v1ll1agvda	290	300	310	320	330	340	350	360	370	380	390	400
I/1b	82	DK11	S-AFTVS-EHHFT-E	I-Q-HIT	L	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	83	83	S-AFTVS-EHHFT-E	I-Q-HIT	L	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	84	T8	S-AFTVS-EHHFT-E	I-Q-HIT	L	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	85	S43	A-MVVS-QHLEVF-E	I-P-TIT	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
I/1a	78	T4	A-MFTVS-QHLEVF-E	I-P-TIT	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	80	US10	A-MFTVS-QHLEVF-E	I-P-TIT	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	79	T9	A-MFTVS-QHLEVF-E	I-P-TIT	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	77	II/2a	A-MFTVS-QHLEVF-E	I-P-TIT	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
I/1b	86	DK12	G-AFTER-RHHTV-T	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	88	US10	G-AFTER-RHHTV-T	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	90	S54	G-AFTER-RHHTV-T	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	89	S52	G-AFTER-RHHTV-T	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
I/1b	68	INB8	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	67	IN5	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	65	H4	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	66	H8	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
I/1b	71	S45	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	69	D3	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	65	H5	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	64	H4	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
I/1b	76	US6	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	75	US10	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	73	T10	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	62	DK1	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
I/1b	70	S9	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	60	D1	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	22	US11	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	55	DR44	S-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
I/1a	54	DR1	G-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	53	DK9	G-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	58	S14	G-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						
	57	S18	G-LFTFS-RHHTV-D	I-P-HVS	M	TMTLLAYAA-V-ELEWVF	G-VFGL-FESMOG-A	-IALLVA	-DA						

FIGURE 4

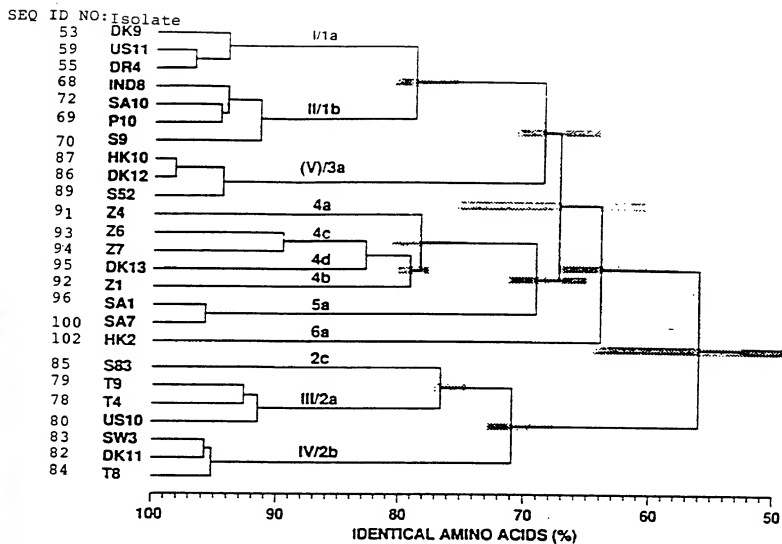


FIGURE 5

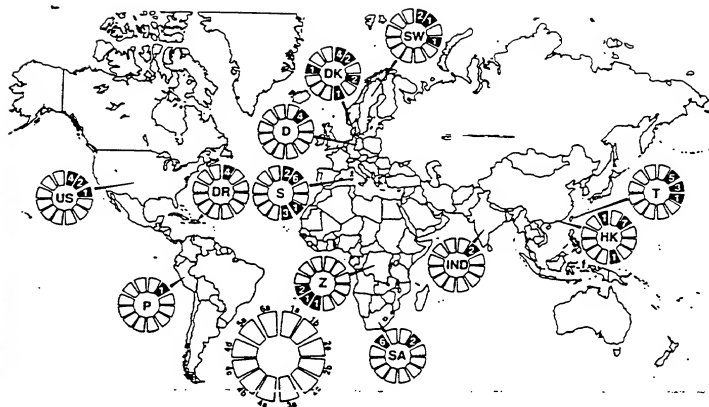


FIGURE 6A

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

1 ATGAGCACGAATCTTAAACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCTTAAACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCTTAAACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCTTAAACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCTTAAACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGG
 1 ATGAGCACGAATCTTAAACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGG

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

ATGAGCACGAATCTTAAACCTCAAAGAAAAACCAACGTAACACCAACCGTCGCCACAGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGTCTGTTGGTGGAGTTTACTTGTGTCGCCGCGAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGTCTGTTGGTGGAGTTTACTTGTGTCGCCGCGAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGTCTGTTGGTGGAGTTTACTTGTGTCGCCGCGAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGTCTGTTGGTGGAGTTTACTTGTGTCGCCGCGAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGTCTGTTGGTGGAGTTTACTTGTGTCGCCGCGAGGGG
 62 ACGTCAAGTTCCCGGGTGGCGGTGAGTCTGTTGGTGGAGTTTACTTGTGTCGCCGCGAGGGG

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

123 CCCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGCAACTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGCGAGGAAGACTTCCGAGCGGTGCGCAACTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGCGAGGAAGACTTCCGAGCGGTGCGCAACTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGCGAGGAAGACTTCCGAGCGGTGCGCAACTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGCGAGGAAGACTTCCGAGCGGTGCGCAACTCGAGGTAGA
 123 CCCTAGATTGGGTGTGCGCGCGCGAGGAAGACTTCCGAGCGGTGCGCAACTCGAGGTAGA

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

184 CGTCAGCCTATCCCCAAGGCgCTGCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGTACC
 184 CGTCAGCCTATCCCCAAGGCACGTGCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGTACC
 184 CGTCAGCCTATCCCCAAGGCACGTGCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGTACC
 184 CGTCAGCCTATCCCCAAGGCACGTGCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGTATC
 184 CGTCAGCCTATCCCCAAGGCAGGTGCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGTATC
 184 CGTCAGCCTATCCCCAAGGCAGGTGCGGCCGAGGGCAGGACCTGGGCTCAGCCCGGTATC

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

245 CTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTC-CCCCGTGG
 245 CTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTC-CCCCGTGG
 245 CTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTC-CCCCGTGG
 245 CTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTC-CCCCGTGG
 245 CTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTC-CCCCGTGG
 245 CTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGCGGGATGGCTCCTGTC-CCCCGTGG

SEQ ID NO: ISOLATE
 108 DR4
 103 DK7
 104 US11
 105 S14
 106 SW1
 107 S18

103-108 consensus

306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTCGCGCAATTTGGGTAAgGTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTCGCGCAATTTGGGTAAgGTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTCGCGCAATTTGGGTAAgGTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTCGCGCAATTTGGGTAAgGTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTCGCGCAATTTGGGTAAgGTC
 306 CTCTCGGCCTAGCTGGGGCCCCACAGACCCCCGGCGtAGGTCGCGCAATTTGGGTAAgGTC

FIGURE 6A

SEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

367 ATCGACACCCTcACGTGCGGCTTCGCCGACCTCATGGGGTACATcCCGCTCGTCGGCGCCCC
367 ATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
367 ATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
367 ATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATACCGCTCGTCGGCGCCCC
367 ATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATTCGGCTCGTCGGCGCCCC
367 ATCGATACCCCTTACGTGCGGCTTCGCCGACCTCATGGGGTACATTCGGCTCGTCGGCGCCCC

ATCGATACCCTcACGTGCGGCTTCGCCGACCTCATGGGGTACATaCCGCTCGTCGGCGCCCC

SEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

428 CcCTTGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGaGTTCTGGAAGACGGCGTGAA
428 CTCTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 CTCTCGSAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 CcCTCGGgGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA
428 CTCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAAGACGGCGTGAA

CtCTcGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGgGTTCTGGAAGACGGCGTGAA

SEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

489 CTATGCAACAGGGAAcCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGCCtTGCTCTCT
489 CTATGCAACAGGGAAcCTTCCTGGTTGCTCTTTCTCTATCTTCCTTTTGCCCTGCTCTCT
489 CTATGCAACAGGGAAcCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCCTGGCCCTGCTCTCT
489 CTATGCAACAGGGAAcCTTCCTGGTTGCTCTTTCTCTATCTTCCTcCTaGCCCTGCTTTCT
489 CTATGCAACAGGGAAcCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCCTGGCCCTGCTTTCT
489 CTATGCAACAGGGAAcCTTCCTGGTTGCTCTTTCTCTATCTTCCTTCCTGGCCCTGCTcTCT

CTATGCAACAGGGAAcCTTCCTGGTTGCTCTTTCTCTATCTTCCTcTgGCCcTGCTcTCT

SEQ ID NO: ISOLATE

108 DR4
103 DK7
104 US11
105 S14
106 SW1
107 S18

103-108 consensus

550 TGcctTGACCGTGCCCGCaTCGGCC
550 TGcCTGACCGTGCCCGCTTCGGCC
550 TGcCTGACTGTGCCCGCTTCAGCC
550 TGcCTGACTGTGCCCGCTTCAGCC
550 TGcCTGACaGTGCCCGCTTCAGCC
550 TGcCTGACTGTGCCCGCTTCAGCc

TGcctTGACTGTGCCCGCtTCaGCc

THE UNIVERSITY OF CHICAGO

ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
1 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
2 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
3 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
4 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
5 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
6 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
7 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
8 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
9 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
10 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
11 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
12 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
13 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
14 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG
15 ATGAGCAGAATTCTAAACCTCAAGAAAAAACCAAACTGTAAACAACCGCCGCCCCACGG

ATGAGCACGAaTCCTAAACCTCAAAGAAaAaACCAAACGTAAACACCAaCCGCCGCCCACAGG

[illegible]

ACGTcAAGTTCCCGGGcGGtGGtCAGATCGTtGGTGGAGTtTAcCTGTTGCCGCGCAGGGG

[illegible]

CCCCaGGTTGGGTGTGCGCGCqACTtAGGAAGACTTCcGAGCGqTCqCAACCTCGTGGaaGG

FIGURE 6B

117	IND3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
118	IND8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
119	D1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
112	US6	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
113	P10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
114	DK1	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
115	T10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
116	SW2	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
122	HK4	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
109	SA10	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
110	S45	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
123	P8	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
124	T3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
120	HK3	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC
121	HK5	184	CGACAACCTATCCCCAAGGCTCGCCGGCCGAGGGTAGGGCTCGGGCTCAGCCCGGGTACC

109-124 consensus CGACAaCCTATCCCCAAGGCTCGCCGGCCGAGGGcAGGgCTTGGGCTCAGCCcGGGTACc

SEQ ID NO:	ISOLATE	
119	S9	245 CTGTGGCCCTCTACGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGtGG
117	IND3	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
118	IND8	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
111	D1	245 CTGTGGCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
112	US6	245 CTGTGGCCCTCTATGGCAACGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
113	P10	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
114	DK1	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
115	T10	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
116	SW2	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
122	HK4	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
109	SA10	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
110	S45	245 CTGTGGCCCTCTATGGCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
123	P8	245 CTGTGGCCCTCTATGcCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
124	T3	245 CTGTGGCCCTCTATGgCgACGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
120	HK3	245 CTGTGGCCCTCTATGgCAACGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG
121	HK5	245 CTGTGGCCCTCTATGgCAATGAGGGCTTGGGGTGGGCAGGATGGCTCTGTCAcCCCGcGG

109-124 consensus CtTGGCCCTCTATGgCAaTgAGGGC - TGGGgTGGGcAGGATGGCTCTGTCAcCCCGcGG

SEQ ID NO:	ISOLATE	
119	S9	306 cTCTCGGCCTAGTTGGGGCCCCAaTgACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
117	IND3	306 tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAaGTC
118	IND8	306 cTCTCGGCCTAGTTGGGGCCCCACAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
111	D1	306 CTCCCGGCCTAGTTGGGGCCCCACaGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
112	US6	306 CTCCCGGCCTAGTTGGGGCCCCACAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
113	P10	306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
114	DK1	306 CTCTCGGCCTAGTTGGGGCCCCAaGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
115	T10	306 CTcCcgGCCTAGTTGGGGCCCCACaGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
116	SW2	306 CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
122	HK4	306 CTCTCGGCCTAGTTGGGGCCCCACGAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
109	SA10	306 CTCTCGGCCTAGTTGGGGCCCCACGAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
110	S45	306 CTCCCGGCCTAGTTGGGGCCCCACGAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
123	P8	306 CTCCCGGCCTAGTTGGGGCCCCACAGGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
124	T3	306 CTCCCGGCCTAAATTGGGGCCCCACaGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
120	HK3	306 CTCTCGGCCTAAATTGGGGCCCCACAGGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC
121	HK5	306 CTCTCGGCCTAgTTGGGGCCCCACGAGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC

109-124 consensus cTCTCGGCCTAgTTGGGGCCCCAcgGACCCCCCGCGCTAGGTCGGCTAAATTGGGTAAgGTC

SEQ ID NO:	ISOLATE	
119	S9	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGGGGTACATcCGCTCGTCGGCGGCCc
117	IND3	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGGGGTACATCCGCTCGTCGGCGGCCc
118	IND8	367 ATCGATACCCCTCACATGCGGCTTcGCCGACCTCATGGGGTACATCCGCTCGTCGGCGGCCc

FIGURE 6B

111	D1	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
112	US6	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
113	P10	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
114	DK1	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
115	T10	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
116	SW2	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
122	HK4	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
109	SA10	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
110	S45	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
123	P8	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
124	T3	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
120	HK3	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
121	HK5	367	ATCGATACCCCTCACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC

109-124 consensus ATCGATACCCCTCACaTGGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGccc

SEQ ID NO:	ISOLATE		
119	S9	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
117	IND3	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
118	IND8	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
111	D1	428	CCCTAGGGGGGTGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
112	US6	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
113	P10	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
114	DK1	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
115	T10	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
116	SW2	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
122	HK4	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
109	SA10	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
110	S45	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
123	P8	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
124	T3	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
120	HK3	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA
121	HK5	428	CCCTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA

109-124 consensus CccTAGGGGGCGCTGCCAGGGCTCTGGCGCATGGCGTCCGGGTCTCGGAGGACGGCGTGAA

SEQ ID NO:	ISOLATE		
119	S9	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTCTgGCTTTGCTgTCC
117	IND3	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTTgGCTTTGCTATCC
118	IND8	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTTgGCTTTGCTATCC
111	D1	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
112	US6	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
113	P10	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
114	DK1	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
115	T10	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
116	SW2	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
122	HK4	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
109	SA10	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
110	S45	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
123	P8	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
124	T3	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
120	HK3	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT
121	HK5	489	CTATGCAACAGGGAACTTCCCGGTTGCTCTTTCTCTATCTTCCTTTGCTTTTgGCTTTGCT

109-124 consensus cTATGCAACAGGGAACTTgCCcGGTTGCTCTTTCTCTATCTTCCTTCTgGCTTTGCTgTCC

SEQ ID NO:	ISOLATE		
119	S9	550	TGTTTGACCATCCAGCTTCCGCT
117	IND3	550	TGTTTGACCATCCAGCTTCCGCT
118	IND8	550	TGTTTGACCATCCAGCTTCCGCT
111	D1	550	TGTTTGACCATCCAGCTTCCGCT
112	US6	550	TGTTTGACCATCCAGCTTCCGCT

FIGURE 6B

113	P10	550	TGcctGACCATCCCAGCgTCCGCT
114	DK1	550	TGTTtTGACCATCCCAGCTTCCGCc
115	T10	550	TGTCTGACCATCCCAGCTTCCGCT
116	SW2	550	TGTCTGACCATCCCAGCTTCCGCT
122	HK4	550	TGTTtTGACCATCCCAGCTTCCGCT
109	SA10	550	TGTTTtAACCATCCCAGCTTCCGCT
110	S45	550	TGcTTGACCATCCCAGCTTCCGCT
123	P8	550	TGtctTGACCATCCCAGCTTCCGCT
124	T3	550	TGCTTGACCATCCCAGCTTCCGCT
120	HK3	550	TGCTTGACCACCCAGCTTCCGCT
121	HK5	550	TGtctGACCACCCAGtTCCGCT
109-124	consensus		TGTTtTgACCatcCCAGctTCCGCT

FIGURE 6C

SEQ ID NO: ISOLATE

119 S9 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 117 IND3 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 118 IND8 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 111 D1 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 112 US6 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 113 P10 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 114 DK1 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 115 T10 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 116 SW2 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 122 HK4 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 109 SA10 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 110 S45 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 123 P8 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 124 T3 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 120 HK3 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 121 HK5 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 108 DR4 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 104 US11 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 105 S14 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 106 SW1 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 107 S18 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG
 103 DK7 1 ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG

103-124 consensus

ATGAGCACGAATCCTAAACCTCAAAGAAAAAACCAAAACGTAACACCAACCGCGCCACAGG

SEQ ID NO: ISOLATE

119 S9 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 117 IND3 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 118 IND8 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 111 D1 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 112 US6 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 113 P10 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 114 DK1 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 115 T10 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 116 SW2 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 122 HK4 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 109 SA10 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 110 S45 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 123 P8 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 124 T3 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 120 HK3 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 121 HK5 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 108 DR4 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 104 US11 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 105 S14 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 106 SW1 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 107 S18 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG
 103 DK7 62 ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG

103-124 consensus

ACGTAAAGTTCGCCGGCGGTGGTCAGATCGTCGTTGGAGTTTACCTGTTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

119 S9 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 117 IND3 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 118 IND8 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 111 D1 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 112 US6 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 113 P10 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 114 DK1 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 115 T10 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 116 SW2 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG
 122 HK4 123 CCCAGGTTGGGTGTGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGAAGG

FIGURE 5C

109 SA10 123 CCCcAGGTTGGGTGTGCGCGCGACgAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGGAAAGG
 110 S45 123 CCCcAGGTTGGGTGTGCGCGCGCACTAGGAAGACTTCCGAGCGGTGcCAACCTCGTGGAGCGG
 123 P8 123 CCCcAGGTTGGGTGTGCGCGCGCACTAGGAAGACTTCCGAGCGATGCGCAACCTCGTGGcAGG
 124 T3 123 CCCcAGGTTGGGTGTGCGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGGGAAGG
 120 HK3 123 CCCcAGGTTGGGTGTGCGCGCGCACTAGGAAGACTTcAGAGCGGTGCGCAACCTCGTGGGAAGG
 121 HK5 123 CCCcAGGTTGGGTGTGCGCGCGCACTAGGAAGACTTCCGAGCGGTGCGCAACCTCGTGGGAAGG
 108 DR4 123 CCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGCAACCTCGAGGTAGA
 104 US11 123 CCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGCAACCTCGAGGTAGA
 105 S14 123 CCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGCAACCTCGAGGTAGA
 106 SW1 123 CCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGCAACCTCGAGGTAGA
 107 S18 123 CCTAGATTGGGTGTGCGCGCGACGAGGAAGACTTCCGAGCGGTGCGCAACCTCGcGGTAGA
 103 DK7 123 CCTAGATTGGGTGTGCGCGCGcCGAGGAAGACTTCCGAGCGGTGCGCAACCTCGaGGTAGA

103-124 consensus CCCcAGgTtGGGTGTGCGCGCGaCtAGGAAGACTTcCGAGCGgTcGcCAACCTCGtGGaaGg

SEQ ID NO: ISOLATE

119 S9 184 CGCAACCTATCCCCAAGGCTCGcCAtCCcGAGGGcAGGGcCTGGGCTCAGCCCGGGTACC
 117 IND3 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 118 IND8 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGcACC
 111 D1 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 112 US6 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 113 P10 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 114 DK1 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 115 T10 184 CGCAAGCTATCCCCAAGGCTCGcCGAGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 116 SW2 184 CGCAACCTATCCCCAAGGCTCGcCGAGCCGAGGGcTAGGGcCTGGGCTCAGCTGGGTACC
 122 HK4 184 CGCAACCTATCCCCAAGGCTCGcCGAaCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 109 SA10 184 CGCAACCTATCCCCAAGGCTCGcCGAGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 110 S45 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGcATc
 123 P8 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGcACC
 124 T3 184 CGCAACCTATCCCCAAGGCTCGcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 120 HK3 184 CGCAACCTATCCCCAAGGCTCGcCaAACCcGAGGGcTAGGGcCTGGGCTCAGCCCGGGTATc
 121 HK5 184 CGCAACCTATCCCCAAGGCTCGcCGAGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 108 DR4 184 CGTcAGCCTATCCCCAAGGcGcGTcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 104 US11 184 CGTcAGCCTATCCCCAAGGcCAcGTcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 105 S14 184 CGTcAGCCTATCCCCAAGGcCAcGTcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTATc
 106 SW1 184 CGTcAGCCTATCCCCAAGGcCGcGTcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTATc
 107 S18 184 CGTcAGCCTATCCCCAAGGcCGcGTcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC
 103 DK7 184 CGTcAGCCTATCCCCAAGGcCaCGTcCGGGCCGAGGGcTAGGGcCTGGGCTCAGCCCGGGTACC

103-124 consensus CGaCAaCCTATCCCCAAGGcTCGcCgGcCCGAGGGcAGGgCTGGGCTCAGCcGGGTACc

SEQ ID NO: ISOLATE

119 S9 245 CTTGGCCCCCTcTAAGGCAATGAGGGcTTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 117 IND3 245 CTTGGCCCCCTcTATGGAATGAGGGcTTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGCGG
 118 IND8 245 CTTGGCCCCCTcTATGGAATGAGGGcTTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGCGG
 111 D1 245 CTTGGCCCCCTcTATGGAACGAGGGcTTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGCGG
 112 US6 245 CTTGGCCCCCTcTATGGAACGAGGGcTaTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 113 P10 245 CTTGGCCCCCTcTATGGAATGAGGGcCTcTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 114 DK1 245 CTTGGCCCCCTcTATGGAATGAGGGcCATGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 115 T10 245 CTTGGCCCCCTcTATGGAATGAGGGcCATGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 116 SW2 245 CcTGGCCCCCTcTATGGAATGAGGGcCATGGGAATGGGcAGGATGgCTcCTGTcACCCcCGCGG
 122 HK4 245 CTTGGCCCCCTcTATGGAATGAGGGcCATGGGGTGGGcAGGATGgCTcCTGTcACCCcCGCGG
 109 SA10 245 CTTGGCCCCCTcTATGGAATGAGGGcCTTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 123 S45 245 CTTGGCCCCCTcTATGGAATGAGGGcCTTGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 123 P8 245 CTTGGCCCCCTcTATGcCAATGAGGGcCTTGGGGTGGGcGgGATGgCTcCTGTcACCCcCGCGG
 124 T3 245 CTTGGCCCCCTcTATGcGcACGAGGGcCATGGGGTGGGcAGGATGgCTcCTGTcACCCcCGCGG
 120 HK3 245 CTTGGCCCCCTcTATGGAACGAGGGcCATGGGGTGGGcAGGATGgCTcCTGTcACCCcCGTGG
 121 HK5 245 CTTGGCCCCCTcTATGGAATGAGGGcCATGGGGTGGGcAGGATGgCTcCTGTcACCCcCATGG
 108 DR4 245 CTTGGCCCCCTcTATGGAATGAGGGcCTGGGGTGGGcGgGATGgCTcCTGTcACCCcCGTGG
 104 US11 245 CTTGGCCCCCTcTATGGAATGAGGGcCTCGGGTGGGcGgGATGgCTcCTGTcACCCcCGTGG
 105 S14 245 CTTGGCCCCCTcTATGGAATGAGGGcCTCGGGTGGGcGgGATGgCTcCTGTcACCCcCGTGG
 106 SW1 245 CTTGGCCCCCTcTATGGAATGAGGGcCTCGGAATGGGcAGGATGgCTcCTGTcACCCcCGTGG
 107 S18 245 CTTGGCCCCCTcTATGGAATGAGGGcCTCGGGTGGGcGgGATGgCTcCTGTcACCCcCGTGG

FIGURE 6C

103 DK7 245 CTTGGCCCCCTCTATGGCAATGAGGGCTGCGGGTGGGCGGGATGGCTCCTGTCTCCCCGTGG
 103-124 consensus CtTGGCCCCCTCTATGgCaAtGAGGGCtTgGgTGGGCaGGATGGCTCCTGTCAcCCcgtGG

SEQ ID NO: ISOLATE
 119 S9 306 cTCTCGGCCTAGTTGGGGCCCCAaTgACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 117 IND3 306 tTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 118 IND8 306 CTCTCGGCCTAGTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 111 D1 306 CTCCCGGCCTAGTTGGGGCCCCACgACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 112 US6 306 CTCCCGGCCTAGTTGGGGCCCCACgACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 113 P10 306 CTCTCGGCCTAGTTGGGGCCCCACgACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 114 DK1 306 CTCTCGGCCTAGTTGGGGCCCCAaCgACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 116 T10 306 CTCCCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 115 SW2 306 CTCTCGGCCTAGTTGGGGCCCCACtGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 122 HK4 306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 109 SA10 306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 110 S45 306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 123 P8 306 CTCCCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 124 T3 306 CTCCCGGCCTAATTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 120 HK3 306 CTCTCGGCCTAATTTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 121 HK5 306 CTCTCGGCCTAGTTGGGGCCCCACGGACCCCCGGCGTAGGTCGCGTAATTTGGGTAAGGTC
 108 DR4 306 CTCTCGGCCTAGTTGGGGCCCCACaGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 104 US11 306 CTCTCGGCCTAGTGGGGCCCCACgACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 105 S14 306 CTCTCGGCCTAGTGGGGCCCCCtACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 106 SW1 306 CTCTCGGCCTAGTGGGGCCCCCtACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 107 S18 306 CTCCCGGCCTAGTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 103 DK7 306 CTCTCGGCCTAGTGGGGCCCCACAGACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC
 103-124 consensus cTCTCGGCCTAgTGGGGCCCCaC- GACCCCCGGCGTAGGTCGCGCAATTTGGGTAAGGTC

SEQ ID NO: ISOLATE
 119 S9 367 ATCGATACCCCTACATGCGGCTTgGCCGACCTCATGGGGTACATcCCGTCGTCGGCGCCC
 117 IND3 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
 118 IND8 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
 111 D1 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCCC
 112 US6 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 113 P10 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 114 DK1 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 115 T10 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 116 SW2 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 122 HK4 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 109 SA10 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 110 S45 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 123 P8 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 124 T3 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 120 HK3 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 121 HK5 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 108 DR4 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 104 US11 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 105 S14 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 106 SW1 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 107 S18 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 103 DK7 367 ATCGATACCCCTACATGCGGCTTCGCCGACCTCATGGGGTACATTCGCTCGTCGGCGCCC
 103-124 consensus ATCGATACCCCTACaTgCGGCTTgGCCGACCTCATGGGGTACATcCCGTCGTCGGCGccc

SEQ ID NO: ISOLATE
 119 S9 428 CCTTAGGGGGCGCTGCCAGGGCtCTGGCGCATGGCGTCCGGGtTCTGGAGGACGGCGTGAA
 117 IND3 428 CCTTAGGGGGCGCTGCCAGGGCCTGGCGCATGGCGTCCGGGtCTGGAGGACGGCGTGAA
 118 IND8 428 CCTTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGtCTGGAGGACGGCGTGAA
 111 D1 428 CCTTAGGGGGTGTGCCAGGGCCCTGGCGCATGGCGTCCGGGtTCTGGAGGACGGCGTGAA
 112 US6 428 CCTTAGGGGGCGCTGCCAGGGCtTGGCGCATGGCGTCCGGGtTCTGGAGGACGGCGTGAA

FIGURE 6C

113 P10 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 114 DK1 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 115 T10 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 116 SW2 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 117 HK4 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 118 HK4 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 119 SA10 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 120 S45 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 121 P8 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 122 T3 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 123 HK3 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 124 HK5 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 125 DR4 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 126 US11 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 127 S14 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 128 SW1 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 129 S18 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 130 DK7 428 CCCTAGGGGGCGCTGCGAGGGCCCTGGCGCATGGCGTCCGGGTTCTGGAGGACGGCGTGAA
 103-124 consensus CccTaGgGgGgGcTgCCAGgGcCctTgGcGcCAtGgCtTCCGgGtTcTGGAGgACGGCGTGAA

SEQ ID NO: ISOLATE

119 S9 489 CTATGCAACAGGGAAcTcCCCGGTGTGCTCTTTCTCTATCTTCCTTcTgGcTTTGCTgTCC
 117 IND3 489 CTATGCAACAGGGAAcTGTCCCGGTGTGCTCTTTCTCTATCTTCCTTTTaGcTTTGCTATCC
 118 IND8 489 CTATGCAACAGGGAAcTGTCCCGGTGTGCTCTTTCTCTATCTTCCTTTTGcCTTTGCTATCC
 111 D1 489 tTATGCAACAGGGAAcTTGCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 112 US6 489 CTATGCAACAGGGAAcTTGCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 113 P10 489 CTATGCAACAGGGAAcTGTCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 114 DK1 489 CTAcGCAACAGGGAAcTTGCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 115 T10 489 CTATGCAACAGGGAAcTTGCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 116 SW2 489 CTATGCAACAGGGAAcTGTCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 122 HK4 489 CTATGCAACAGGGAAcTTGCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 123 SA10 489 CTATGCAACAGGGAAcTTGCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 110 S45 489 CTATGCAACAGGGAAcTGTCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 123 P8 489 CTATGCAACAGGGAAcTGTCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 124 T3 489 tTAcGCAACAGGGAAcTTGCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 120 HK3 489 CTATGCAACAGGGAAcTTAcCCCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCTTTGCTGTCC
 121 HK5 489 CTAcGCAACAGGGAAcTaTCCCGGTGTGCTCTTTCTCTATCTTCCTTTTGcCTTTGCTGTCC
 122 DR4 489 CTATGCAACAGGGAAcTTCTCGGTGTGCTCTTTCTCTATCTTCCTTTTGcCTTTGCTGTCTCT
 124 US11 489 CTATGCAACAGGGAAcCTTCTCGGTGTGCTCTTTCTCTATCTTCCTTTTGcCTTTGCTGTCTCT
 105 S14 489 CTATGCAACAGGGAAcCTTCTCGGTGTGCTCTTTCTCTATCTTCCTcTaGcCCTGTCTTTCT
 106 SW1 489 CTATGCAACAGGGAAcCTTCTCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCCTGTCTTTCT
 107 S18 489 CTATGCAACAGGGAAcCTTCTCGGTGTGCTCTTTCTCTATCTTCCTCTTGcCCTGTCTCTCT
 108 DK7 489 CTATGCAACAGGGAAcCTTCTCGGTGTGCTCTTTCTCTATCTTCCTTTTGcCCTGTCTCTCT
 103-124 consensus cTATGCAACAGGGAAcTgCCcGGTGTGcTcTtTcTCTATCTTCCTcTgTgCctTgCtTgTCC

SEQ ID NO: ISOLATE

119 S9 550 TgTTTgACCATCCcAGcTTCCGCT
 117 IND3 550 TgTTTgACCATCCcAGcTTCCGCT
 118 IND8 550 TgTTTgACcGTCCcAGcTTCCGCT
 111 D1 550 TgTTTgACCATCCcAGcTTCCGCT
 112 US6 550 TgTTTgACCATCCcAGcTTCCGCT
 113 P10 550 TgCcTgACCATCCcAGcTTCCGCT
 114 DK1 550 TgTtTgACCATCCcAGcTTCCGcC
 115 T10 550 TgTCTgACCATCCcAGcTTCCGCT
 116 SW2 550 TgTCTgACCATCCcAGcTTCCGCT
 122 HK4 550 TgTTTgACCATCCcAGcTTCCGCT
 109 SA10 550 TgTTTtAACCATCCcAGcTTCCGCT
 110 S45 550 TgCcTgACCATCCcAGcTTCCGCT
 123 P8 550 TgTcTgACCATCCcAGcTTCCGCT
 124 T3 550 TgCTTgACCATCCcAGcTTCCGCT
 120 HK3 550 TgCTTgACcACCCcAGcTTCCGCT
 121 HK5 550 TgTcTgACcACCCcAGcTTCCGCT

FIGURE 6C

108	DR4	550	TGctTGACCGTGCCCGCaTCgGCC
104	US11	550	TGCCTGACTGTGCCCCGCTTCAGCC
105	S14	550	TGCCTGACTGTGCCCCGCTTCAGCC
106	SW1	550	TGCCTGACaGTGCCCCGCTTCAGCC
107	S18	550	TGctTGACTGTGCCCCGCTTCAGCt
103	DK7	550	TGCCTGACcGTGCCCCGCTTCgGCC
103-124	consensus		TGtTgACcatcCCaGctTCcGCT

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted March 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

FIGURE 6D

SEQ ID NO:	ISOLATE	
128	T2	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAACAC - AACCGTCGCCACaG
125	T4	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAACAC - AACCGTCGCCACaG
126	US10	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAACAC - AACCGTCGCCACaG
127	T9	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAACAC - AACCGTCGCCACaG
125-128	consensus	ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAACAC - AACCGTCGCCACaG
SEQ ID NO:	ISOLATE	
128	T2	62 ACGTTAAGTTTCCGGGCGCGCGCAGATCGTTGGCGGAGTATACTTGTGCGCGCAGGGG
125	T4	62 ACGTTAAGTTTCCGGGCGCGCGCAGATCGTTGGCGGAGTATACTTGTGCGCGCAGGGG
126	US10	62 ACGTTAAGTTTCCGGGCGCGCGCAGATCGTTGGCGGAGTATACTTGTGCGCGCAGGGG
127	T9	62 ACGTTAAGTTTCCGGGCGCGCGCAGATCGTTGGCGGAGTATACTTGTGCGCGCAGGGG
125-128	consensus	ACGTTAAGTT - CCGGGCGCGCGCAGATCGTTGGCGGAGTATACTTGTGCGCGCAGGGG
SEQ ID NO:	ISOLATE	
128	T2	123 CCCAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGgTCCAGCCTCGTGGaAGG
125	T4	123 CCCAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGaTCCAGCAGCTGGGAGG
126	US10	123 CCCAGGTTGGGTGTGCGCGGACAAGGAAGACTTCGGAGCGGTCCAGCAGCTGGGAGG
127	T9	123 CCTCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCGGAGCGGTCCAGCAGCTGGGAGG
125-128	consensus	CCCAGGTTGGGTGTGCGGgCGACAAGGAAGACTTCGGAGCGgTCCAGCcaCGTGGgAGG
SEQ ID NO:	ISOLATE	
128	T2	184 CGCGAGCCCATCCCTAAAGATCGGCGCTCCACTGGCAAGTCTGGGGAAAAACAGGATAcC
125	T4	184 CGCGAGCCCATCCCAAGATCGGCGCTCCACTGGCAAGTCTGGGGAAAAACAGGATAcC
126	US10	184 CGCGAGCCCATCCCAAGATCGGCGCcCACTGGCAAGTCTGGGGAAAAACAGGATAcC
127	T9	184 CGCGAGCCCATCCCAAGATCGGCGCTCCACTGGCAAGTCTGGGGAAAAACAGGATAcC
125-128	consensus	CGCGAGCCCATCCcAAAGATCGGCGctCCACTGGCAAGTCTGGGGAAAAACAGGATAcC
SEQ ID NO:	ISOLATE	
128	T2	245 CTTGGCCCCCTGTATGGGAATGAGGGgCTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
125	T4	245 CTTGGCCCCCTGTATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
126	US10	245 CtTGGCCCCCTATATGGGAATGAGGGACTCGGCTGGGCAGGATGGCTCCTGTCCCCCGAGG
127	T9	245 CctTGGCCcCTATATGGGAATGAGGGACTCGGCTGGGcGGATGGCTCCTGTCCCCCGAGG
125-128	consensus	CctTGGCCcCT - TATGGGAATGAGGgACTCGGCTGGGcAGGATGGCTCCTGTCCCCCGAGG
SEQ ID NO:	ISOLATE	
128	T2	306 TTCTCGTCCCTCtTGGGGCCCCAATGACCCCCGGCATAGGTCGCGCAAcGTGGGTAAgSTC
125	T4	306 TTCCCGTCCCTCctTGGGGCCCCAATGACCCCCGGCATAGGTCGCGCAACGTGGGTAAgSTC
126	US10	306 TTCCCGTCCCTCTTGGGGCCCCAcTgATcCCCGCATAGGTCGCGCAACGTGGGTAAgSTC
127	T9	306 TTCCCGTCCCTCTTGGGGCCCCAgTGAcCCCGCATAGGTCGCGCAACGTGGGTAAgSTC
125-128	consensus	TTCTCGTCCCTCtTGGGGCCCCAaTGAcCCCGCATAGGTCGCGCAAcGTGGGTAAgSTC
SEQ ID NO:	ISOLATE	
128	T2	367 ATCGATACCCCTAACGTGCGgGctTTGCCGACCTCATGGGGTACaTCCCCGTCGTAGGCGcCC
125	T4	367 ATCGATACCCCTAACGTGCGaGcctTTGCCGACCTCATGGGGTACgTCCCCGTCGTAGGCGcCC
126	US10	367 ATCGATACCCCTAACGTGCGGCTTTGCCGACCTCATGGGATACATCCCCGTCGTAGGCGcctC
127	T9	367 ATCGATACCCCTAACGTGCGGCTTTGCCGACCTCATGGGgTACATCCCCGTCGTAGGCGcC
125-128	consensus	ATCGATACCCCTAACGTGCGgGctTTGCCGACCTCATGGGgTACaTCCCCGTCGTAGGCGcC
SEQ ID NO:	ISOLATE	
128	T2	428 CGcTtGGTgTGTGCGCAGAGCTCTtGCGCATGGCGTGAGAGTCTCGGAGGACGGaGTTAA

FIGURE 6D

125	T4	428	CGtTgGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGAGTCCTGGAGGACGGGGTTAA
126	US10	428	CGCTTGGTGGCGTCGCCAGAGCTCTCGCGCATGGCGTGAGgGTCTTGGAGGACGGGGTTAA
127	T9	428	CGCTTGGTGGCGTtGCCAGAGCTCTCGCGCAcGGCGTGAGaGTCTTGGAGGACGGGGTTAA
125-128	consensus		CGcTtGGTGGcGTcGCCAGAGCTCTcCGGCAtGGCGTGAGaGTCTTGGAGGACGGgGTTAA

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	489
125	T4	489
126	US10	489
127	T9	489
125-128	consensus	

TTATGCAACAGGtAACTTACCcGGTTGCTCCTTTTCTATcTTCTTGCTaGCCCTgCTGTCC
TTATGCAACAGGGAACTTACCtGGTTGCTCCTTTTCTATcTTCTTGCTGGCCCTACTGTCC
TTATGCAACAGGGAACTTACCcGGTTGCTCCTTTTCTATCTTCTTGCTGGCCcTACTGTCC
TTATGCAACAGGGAAcTACCtGGTTGCTCtTTTTCTATCTTCTTGCTGGCCcTACTGTCC
TTATGCAACAGGgAAcTACC-GGTTGCTCcTTTTCTATcTTCTTGCTgGCCcTaCTGTCC

<u>SEQ ID NO:</u>	<u>ISOLATE</u>	
128	T2	550
125	T4	550
126	US10	550
127	T9	550
125-128	consensus	

TGCATCACTaATTCCgGTtTCaGCT
TGCATCACCAATTCCAGTCTCcGCT
TGCATCACCAATTCCAGTCTCTGCT
TGCATCACCAcTCCgGcCTCTGCT
TGCATCACcAtTCC-GtcTcGCT

FIGURE 6E

SEQ ID NO:	ISOLATE	
131	DK11	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAATACAAACCGCCGCCACAGG
132	SW3	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAATACAAACCGCCGCCACAGG
133	DK8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAATACAAACCGCCGCCACAGG
129	T8	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAATACAAACCGCCGCCACAGG
130	US1	1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAATACAAACCGCCGCCACAGG
129-133	consensus	ATGAGCACAAATCCTAAACCTCAAAGAAAAACAAAAGAAATACAAACCGCCGCCACAGG
131	DK11	62 ACGTTAAGTTCCTCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTTGTCTGCCGCGCAGGGG
132	SW3	62 ACGTTAAGTTCCTCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTTGTCTGCCGCGCAGGGG
133	DK8	62 ACGTTAAGTTCCTCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTTGTCTGCCGCGCAGGGG
129	T8	62 ACGTTAAGTTCCTCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTTGTCTGCCGCGCAGGGG
130	US1	62 ACGTTAAGTTCCTCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTTGTCTGCCGCGCAGGGG
129-133	consensus	ACGTTAAGTTCCTCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTTGTCTGCCGCGCAGGGG
131	DK11	123 CCCAGGTTGGGTGTGCGCaCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCTGGGAGA
132	SW3	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCTGGGAGA
133	DK8	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGTCTTCCGAGCGATCCCAGCCGCTGGGAGg
129	T8	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCTGGGAGA
130	US1	123 CCCAGGTTGGGTGTGCGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCTGGGAGA
129-133	consensus	CCCAGGTTGGGTGTGCGCGACAAGGAAGACTTCCGAGCGATCCCAGCCGCTGGGAGA
131	DK11	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGcCTTGGGAAAGCCAGGATATC
132	SW3	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC
133	DK8	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCgGATATC
129	T8	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC
130	US1	184 CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC
129-133	consensus	CGCCAGCCCCATCCCGAAAGATCGGCGCTCCACCGGCAAGTCTTGGGAAAGCCAGGATATC
131	DK11	245 CTTGGCCCCCTGTATGSAACGAGGGCTGCGGCTGGGcAGGTTGGCTCTGTCCCCCGCGG
132	SW3	245 CTTGGCCCCCTGTATGSAACGAGGGCTGCGGCTGGGcAGGTTGGCTCTGTCCCCCGCGG
133	DK8	245 CTTGGCCCCCTGTATGSAACGAGGGCTGCGGCTGGGcAGGTTGGCTCTGTCCCCCGCGG
129	T8	245 CTTGGCCCCCTGTATGSAACGAGGGCTGCGGCTGGGcAGGTTGGCTCTGTCCCCCGCGG
130	US1	245 CTTGGCCCCCTGTATGSAACGAGGGCTGCGGCTGGGcAGGTTGGCTCTGTCCCCCGCGG
129-133	consensus	CTTGGCCCCCTGTATGSAACGAGGGCTGCGGCTGGGcAGGTTGGCTCTGTCCCCCGCGG
131	DK11	306 GTCTCATCTCTAAATTGGGGCCCCACTGACCCCCGGCATAaATCAGCAATTTGGGcAAAGTC
132	SW3	306 GTCTCATCTCTAAATTGGGGCCCCACTGACCCCCGGCATAAGATCAGCAATTTGGGcAAAGTC
133	DK8	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCATAAGATCAGCAATTTGGGcAAAGTC
129	T8	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCATAAGATCAGCTAAATTGGGcAGAGTC
130	US1	306 GTCTCGTCTACTTTGGGGCCCCACTGACCCCCGGCATAAGATCAGCTAAATTGGGcAGAGTC
129-133	consensus	GTCTCgTCTAcTTGGGGCCCCACTGACCCCCGGCATAgATCAGCgAAATTGGGcAaaGTC
131	DK11	367 ATCGACACCATTACGTGTGGTTTTTGCCGACCTCATGGGTACATCCCTGTCTGcGGCGCCC
132	SW3	367 ATCGACACCATTACGTGTGGTTTTTGCCGACCTCATGGGTACATCCCTGTCTGcGGCGCCC
133	DK8	367 ATCGACACCATTACGTGTGGTTTTTGCCGACCTCATGGGTACATCCCTGTCTGcGGCGCCC
129	T8	367 ATCGATACCAATTACaTGTGGTTTTTGCCGACCTCATGGGTACATCCCTGTCTGcGGCGCCC

FIGURE 6E

130	US1	367	ATCGATACCATTTACgTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTGCTTGGCGCCC
129-133	consensus		ATCGAcACCATTTACgTGTGGTTTTGCGGACCTCATGGGGTACATCCCTGTGCTtGGCGCCC
<u>SEQ ID NO:</u> <u>ISOLATE</u>			
131	DK11	428	CGGTcGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
132	SW3	428	CGGTcGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGAGTCCTGGAAGACGGGATAAA
133	DK8	428	CGGTtGGAGGCGTCGCCAGAGCTCTGGCACACGGTGTTAGGGTCCTGGAAGACGGGATAAA
129	T8	428	CGGTcGGAGGCGTCGCCAGAGCTCTGGCACAtGGTGTTAGGGTCCTGGAAGACGGGATAAA
130	US1	428	CGGTcGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGGGTCCTGGAAGACGGGATAAA
129-133	consensus		CGGTcGGAGGCGTCGCCAGAGCTCTGGCACAcGGTGTTAGgTCTCTGGAAGACGGGATAAA
<u>SEQ ID NO:</u> <u>ISOLATE</u>			
131	DK11	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGCTCTTCTGTCa
132	SW3	489	TTACGCAACAGGGAATCTGCCTGGTTGCTCTTTTCTATCTTCTTACTTGCTCTTCTGTGCG
133	DK8	489	TTACGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTCTTGCTTGCTCTTCTGTGCG
129	T8	489	cTAtGCAACAGGGAATTTGCCTGGTTGCTCTTTTCTATCTTCTTGCTTGCTCTTCTGTCa
130	US1	489	tTAcGCAACAGGGAATcTGCCTGGTTGCTCctTTTCTATCTTCTTaCTTGCTCTTCTGTGcg
129-133	consensus		tTAcGCAACAGGGAATcTGCCTGGTTGCTCctTTTCTATCTTCTTaCTTGCTCTTCTGTGcg
<u>SEQ ID NO:</u> <u>ISOLATE</u>			
131	DK11	550	TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550	TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550	TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550	TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550	TGCGcCACgGTGCCgGTGTCTGCA
129-133	consensus		TGCTt-CACaGTGCCaGTGTCTGcg

FIGURE 6F

SEO ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8C
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAATACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAACCGCGCCACAGG
1 ATGAGCACAAATCCTAAACCTCAAAGAAAAACCAAAGAAACACAACCGCGCCACAGG

SEO ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

62 ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGTGGCGGTCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG

ACGTTAAGTTCCCGGGTGGCGGCAGATCGTTGGCGGAGTTTACTGTGTCGCGCGCAGGGG

SEO ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

123 CCCAGGTTGGGTGTGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA
123 CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA

CCCAGGTTGGGTGTGCGCGCGCACAAAGGAAGACTTCCGAGCGATCCAGCGCGTGGGAGA

SEO ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8
130 US1
125 T4
126 US10
127 T9
128 T2
134 S83

125-134 consensus

184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC
184 CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC

CGCCAGCCCATCCCGAAAGATCGGCGCTCCACGGCAGCTCTGGGAAAGCAGGATATC

SEO ID NO: ISOLATE

131 DK11
132 SW3
133 DK8
129 T8

245 CTTGGCCCTCTGTATGGAACAGAGGGCTGCGGCTGGGCAGGTTGGCTCTGTCTCCCGCGG
245 CTTGGCCCTCTGTATGGAACAGAGGGCTGCGGCTGGGCAGGTTGGCTCTGTCTCCCGCGG
245 CTTGGCCCTCTGTATGGAACAGAGGGCTGCGGCTGGGCAGGTTGGCTCTGTCTCCCGCGG
245 CTTGGCCCTCTGTATGGAACAGAGGGCTGCGGCTGGGCAGGTTGGCTCTGTCTCCCGCGG

FIGURE 6P

130 US1 245 CTGGCCCTCTGTACGGAACGAGGGCTCGGCTGGGCGAGGTTGGCTCTGTCCCCCGCGG
 125 T4 245 CTGGCCCTCTGTATGGGAATGAGGGAGCTCGGCTGGGCGAGGATGGCTCTGTCCCCCGAGG
 126 US10 245 CTGGCCCTCTATATGGGAATGAGGGAGCTCGGCTGGGCGAGGATGGCTCTGTCCCCCGAGG
 127 T9 245 CTGGCCCTCTATATGGGAATGAGGGAGCTCGGCTGGGCGAGGATGGCTCTGTCCCCCGAGG
 128 T2 245 CTGGCCCTCTGTATGGGAATGAGGGAGCTCGGCTGGGCGAGGATGGCTCTGTCCCCCGAGG
 134 S83 245 CTGGCCCTCTGTATGGGAATGAGGGAGCTCGGCTGGGCGAGGATGGCTCTGTCCCCCGAGG

125-134 consensus CTTGGCCCTGTATGG-AA-GAGGGc--CGGcTGGGCaGGTGGCTCTGTCCCCCGcGG

SEO ID NO: ISOLATE

131 DK11 306 GTCTCATCTTAATTGGGGCCCCACTGACCCCGGCATAAATCAGCAATTTGGGTAAGGTC
 132 SW3 306 GTCTCATCTTAATTGGGGCCCCACTGACCCCGGCATAGATCAGCAATTTGGGCAAGTC
 133 DK8 306 GTCTCGTCTTACTTTGGGGCCCCACTGACCCCGGCATAGATCAGCAATTTGGGCAAGTC
 129 T8 306 GTCTCGTCTTACTTTGGGGCCCCACTGACCCCGGCATAGATCAGTAATTTGGGCAAGTC
 130 US1 306 GTCTCGTCTTACTTTGGGGCCCCACTGACCCCGGCATAGATCAGTAATTTGGGCAAGTC
 125 T4 306 TTCCCGTCCCTCTTTGGGGCCCCAaTGACCCCGGCATAGGTCGCGCAAGCTGGGTAAGGTC
 126 US10 306 TTCCCGTCCCTCTTTGGGGCCCCAaTGATCCCCCGGCATAGGTCGCGCAAGCTGGGTAAGGTC
 127 T9 306 TTCCCGTCCCTCTTTGGGGCCCCAaTGACCCCGGCATAGGTCGCGCAAGCTGGGTAAGGTC
 128 T2 306 TTCTCGTCCCTCTTTGGGGCCCCAaTGACCCCGGCATAGGTCGCGCAaGTGGGTAaAGTC
 134 S83 306 TTCTCGCCCTcTATGGGGCCCCAccGACCCCGGCATAAaTCGCGCAaTtGGGTAAGGTC

125-134 consensus -TcTcgtCCt-ctTGGGGCCCCActGACCCCGGCATAgATc-CGcAA-tTGGGTAa-GTC

SEO ID NO: ISOLATE

131 DK11 367 ATCGACACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTcGGCGCCC
 132 SW3 367 ATCGACACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 133 DK8 367 ATCGACACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 129 T8 367 ATCGATACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 130 US1 367 ATCGATACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 125 T4 367 ATCGATACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 126 US10 367 ATCGATACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 127 T9 367 ATCGATACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 128 T2 367 ATCGATACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC
 134 S83 367 ATCGATACCATTTACGTGTGGTTTTTGCCGACCTCATGGGGTACATCCCTGTGCTGGCGCCC

125-134 consensus ATCGATACC-T-ACGTG-gGtTTTGCCGACCTCATGGGGTACATcCC-GTCGtTGGCGccC

SEO ID NO: ISOLATE

131 DK11 428 CGGTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTTAGAGTCTCTGGAAGACGGGATAAA
 132 SW3 428 CGGTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTTAGAGTCTCTGGAAGACGGGATAAA
 133 DK8 428 CGGTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTTAGAGTCTCTGGAAGACGGGATAAA
 129 T8 428 CGGTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTTAGAGTCTCTGGAAGACGGGATAAA
 130 US1 428 CGGTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTTAGAGTCTCTGGAAGACGGGATAAA
 125 T4 428 CGGTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTTAGAGTCTCTGGAAGACGGGATAAA
 126 US10 428 CGGTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTTAGAGTCTCTGGAAGACGGGATAAA
 127 T9 428 CGCTTGGTGGCGTcGCCAGAGCTCTCGGCGcAGGGCTGAGAGTCTCGGAGACGGGGTTAA
 128 T2 428 CGCTTGGTGGTcGTcGCCAGAGCTCTcGGCGcATGGCGTGAAGTCTCGGAGACGGGGTTAA
 134 S83 428 CcgtTGGcGGcGTcGCCAGAGcCTcGcCCATGGgGTGAGgGtTCTGAGGACGGGgTAaAA

125-134 consensus CggTcGAGGcGTcGCCAGAGcCTcTgGcAcA-GgtGT-AG-GTcTGGa-GACGGgTAaAA

SEO ID NO: ISOLATE

131 DK11 489 TTACGCAACAGGGAATCTGCCTGGTGTCTCTTTCTATCTCTTACTTGCTCTCTGTGTCa
 132 SW3 489 TTACGCAACAGGGAATCTGCCTGGTGTCTCTTTCTATCTCTTACTTGCTCTCTGTGTCG
 133 DK8 489 TTACGCAACAGGGAATTTGCCCTGGTGTCTCTTTCTATCTCTTACTTGCTCTCTGTGTCG
 129 T8 489 cTATGCAACAGGGAATTTGCCCTGGTGTCTCTTTCTATCTCTTACTTGCTCTCTGTGTCa
 130 US1 489 TTAcGCAACAGGGAATcTGcCTGGTGTCTCTTTCTATCTCTTAcTGTCTCTCTGTGTCg
 125 T4 489 TTATGCAACAGGGAACCTTACCcGGTGTCTCTTTCTATcTTCTTGCTGGcCTACTGTCC
 126 US10 489 TTATGCAACAGGGAACCTTACCcGGTGTCTCTTTCTATcTCTTGCTGGcCTACTGTCC
 127 T9 489 TTATGCAACAGGGAACcTACCcGGTGTCTCTTTCTATcTCTTGCTGGcCTACTGTCC
 128 T2 489 TTATGCAACAGGGAACCTTACCcGGTGTCTCTTTCTATcTCTTGCTGaCCCTGTGTCc

FIGURE 6P

134	S83	489	TTATGCAACgGGgAAcTTgCCCGTTGCTCtTtTCTATCTTtcTctTgGCCCTctTGTCTc
125-134	consensus		tTAtGCAACaGGgAAcTtTgCcTGGTTGCTCtTtTCTATcTTctTgcTtGC-cTtcTGTCC

SEQ ID NO:	ISOLATE		
131	DK11	550	TGCTgCACAGTGCCAGTGTCTGCG
132	SW3	550	TGCTtCACAGTGCCAGTGTCTGCG
133	DK8	550	TGCTgCACAGTGCCAGTGTCTGCG
129	T8	550	TGCTtCACAGTGCCAGTGTCTGCA
130	US1	550	TGCgcCACgGTGCCgGTGCTGCA
125	T4	550	TGCATCACCATTCcAGTCTCcGCT
126	US10	550	TGCATCACCATTCcAGTCTCTGCT
127	T9	550	TGCATCACCAcTCCGGeCTCTGCT
128	T2	550	TGCATCACTATTCCGGTTTCaGCT
134	S83	550	TGCATCtCTgTgCCaGTTTCcGcC
125-134	consensus		TGCatCaCagtGCCaGtgTcTcGcT

131
132
133
129
130
125
126
127
128
134

FIGURE 6G

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCACAGG
1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCACAGG
1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCACAGG
1 ATGAGCACACTTCCTAAACCTCAAAGAAAAACCAAAGAAACACCATCCGTCGCCACAGG

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

62 ACGTCAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
62 ACGTTAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG
62 AcaTCAAGTTCCCGGGTGGCGGACAGATCGTTGGTGGAGTATACGTGTTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

123 CCCACGATTGGGTGTGCGCGCAGCGCTAAAACTTCTGAACGGTCAcAGCCTCGCGGACGg
123 CCCACGATTGGGTGTGCGCGCAGCGCTAAAACTTCTGAACGGTCAcAGCCTCGCGGACGg
123 CCCACGATTGGGTGTGCGCGCAGCGCTAAAACTTCTGAACGGTCAcAGCCTCGCGGACGg
123 CCCACGATTGGGTGTGCGCGCAGCGCTAAAACTTCTGAACGGTCAcAGCCTCGCGGACGg

CCCACGATTGGGTGTGCGCGCAGCGCTAAAACTTCTGAACGGTCAcAGCCTCGCGGACG-

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCGGTCCTGGGCTCAGCCtGGGTACC
184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCGGTCCTGGGCTCAGCCCGGGTACC
184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCGGTCCTGGGCTCAGCCCGGGTACC
184 CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCGGTCCTGGGCTCAGCCCGGGTACC

CGACAGCCTATCCCCAAGGCGCGTCGGAGCGAAGGCGGTCCTGGGCTCAGCCCGGGTACC

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

245 CTTGGCCCCCTCTATGTTAAcGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
245 CTTGGCCCCCTCTATGTTAAcGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
245 CTTGGCCCCCTCTATGTTAAcGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG
245 CTTGGCCCCCTCTATGTTAAcGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG

CTTGGCCCCCTCTATGTTAAcGAGGGCTGCGGGTGGGcAGGgTGGCTCCTGTCCCCACGCGG

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

306 CTCCCGTCCATCTTGGGGCCCCAAACGACCCCGGCGgaGGTCCGCAATTTGGGTAAgGTC
306 CTCCCGTCCATCTTGGGGCCCCAAACGACCCCGGCGgaGGTCCGCAATTTGGGTAAAGTC
306 CTCCCGTCCATCTTGGGGCCCCAAACGACCCCGGCGAGGTCCCGCAATTTGGGTAAAGTC
306 CTCCCGTCCATCTTGGGGCCCCAAAcGACCCCGGCGAGGTCCCGCAATTTGGGTAAAGTC

CTCCCGTCCATCTTGGGGCCCCAAAcGACCCCGGCGgaGGTCCGCAATTTGGGTAAAgGTC

SEQ ID NO: ISOLATE

138 DK12
135 HK10
136 S52
137 S2

135-138 consensus

367 ATCGATACCCCTcACGTGCGGgATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
367 ATCGATACCCCTTACGTGCGGgATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
367 ATCGATACCCCTTACGTGCGGgATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC
367 ATCGATACCCCTTACGTGCGGgATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC

ATCGATACCCCTcACGTGCGGgATTCGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGCTC

SEQ ID NO: ISOLATE

138 DK12

428 CtGTAGGgGGCGTCGAAGAGCCCTCGCGCATGGCTGAGGGCCCTTGAAGACGGGATAAA

FIGURE 6G

135	HK10	428	CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
136	S52	428	CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
137	S2	428	CCGTAGGAGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
135-138 consensus			CcGTAGGaGGCGTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTTGAAGACGGGATAAA
<u>SEO ID NO: ISOLATE</u>			
138	DK12	489	TTTCGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCT
135	HK10	489	TTTCGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCT
136	S52	489	TTTTGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCTc
137	S2	489	TTTTGCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCTc
135-138 consensus			TTT-GCAACAGGGAACCTTGCCCGGTTGCTCCTTTTCTATCTTCCTTCTTGCTCTGTTCTCTc
<u>SEO ID NO: ISOLATE</u>			
138	DK12	550	TGCCtTAATTcATCCaGCAGCTAGT
135	HK10	550	TGCTTAATTcATCCaGCAGCTAGT
136	S52	550	TGCTTAATTcATCCaGCAGCTAGT
137	S2	550	TGCTTAATTcATCCaGCAGCTAGT
135-138 consensus			TGCTTAATTcATCCaGCAGCTAGT

FIGURE 6H

SEQ ID NO: ISOLATE

145 DK13
143 26
144 27
140 28
139 24
142 25
141 21

139-145 consensus

1 ATGAGCAGCAATCTTAACCTCAAAGAAAAACCAACGTAACCAACCCGCCATGG
1 ATGAGCAGCAATCTTAACCTCAAAGAAAAACCAACGTAACCAACCCGCCATGG
1 ATGAGCAGCAATCTTAACCTCAAAGAAAAACCAACGTAACCAACCCGCCATGG
1 ATGAGCAGCAATCTTAACCTCAAAGAAAAACCAACGTAACCAACCCGCCATGG
1 ATGAGCAGCAATCTTAACCTCAAAGAAAAACCAACGTAACCAACCCGCCATGG
1 ATGAGCAGCAATCTTAACCTCAAAGAAAAACCAACGTAACCAACCCGCCATGG

ATGAGCAGCAATCTTAACCTCAAAGAAAAACCAACGTAACCAACCCGCCATGG

SEQ ID NO: ISOLATE

145 DK13
143 26
144 27
140 28
139 24
142 25
141 21

139-145 consensus

62 ACGTTAAGTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTTAAGTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTTAAGTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTTAAGTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTTAAGTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTTAAGTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG
62 ACGTTAAGTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG

ACGT-AAgTTCCTCCGGGTGGCGCGCAGATCGTTGGCGAGTTTACTTGTGTGCCGCGCAGGGG

SEQ ID NO: ISOLATE

145 DK13
143 26
144 27
140 28
139 24
142 25
141 21

139-145 consensus

123 CCCTAGATTGGGTGTGCGCGGACTAGGAAGACTTCGAGCGGTGCGCAACTCGTGGGAGG
123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCGAGCGGTGCGCAACTCGTGGGAGG
123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCGAGCGGTGCGCAACTCGTGGGAGG
123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCGAGCGGTGCGCAACTCGTGGGAGG
123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCGAGCGGTGCGCAACTCGTGGGAGG
123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCGAGCGGTGCGCAACTCGTGGGAGG
123 CCCAGGTTGGGTGTGCGCGGACTAGGAAGACTTCGAGCGGTGCGCAACTCGTGGGAGG

CCCcAGgTTGGGTGTGCGCGGcGgCaTcGgAAGACTTCGAGCGGTGCGCAACTCGTGGGAGg

SEQ ID NO: ISOLATE

145 DK13
143 26
144 27
140 28
139 24
142 25
141 21

139-145 consensus

184 CGCCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC
184 CGCCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC
184 CGTCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC
184 CGTCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC
184 CGTCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC
184 CGTCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC
184 CGTCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC

CGTCAGCCTATCCCCAAGGCGCGcCaActcGAGGGTAgGTCTCGGGCTCAGCCtGGGTATC

SEQ ID NO: ISOLATE

145 DK13
143 26
144 27
140 28
139 24
142 25
141 21

139-145 consensus

245 CtTGGCCcCTTTAcGGcAATGAGGcTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG
245 CATGGCCCTTTAcGGTAAAGAGGTTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG
245 CATGGCCCTTTAcGGTAAAGAGGTTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG
245 CATGGCCCTTTAcGGTAAAGAGGTTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG
245 CATGGCCCTTTAcGGTAAAGAGGTTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG
245 CATGGCCCTTTAcGGTAAAGAGGTTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG
245 CATGGCCCTTTAcGGTAAAGAGGTTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG

CtTGGCCcCTTTAcGGcAATGAGGcTGCGGTGGGCGGATGGCTCTGTCAACCCCGTGG

SEQ ID NO: ISOLATE

145 DK13
143 26
144 27
140 28

306 CTCTCGGCGGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAAGTTC
306 CTCTCGGCGGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAAGTTC
306 CTCTCGGCGGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAAGTTC
306 CTCTCGGCGGTCTTGGGGcCCgAATGATCCCCGGCGgAGGTCCCGCAACTTGGGTAAAGTTC

FIGURE 6H

139	Z4	306	CTCTCGGCCATCTTGGGGCCCAATGATCCCCGGCGGAGATCGCGCAATCTGGGTAAGGTC
142	Z5	306	aTCTCGGCCATCTTGGGGCCCAAAATGATCCCCGGCGTAGTCCCCCAATCTGGGTAAGGTC
141	Z1	306	tTcCaGGCCgTCTTGGGGCCcAAATGATCCCCGGCGTAGTCCCGtAAATCTGGGTAAGGTC

139-145 consensus cTCTcGcGcGCTCTTGGGGcCcaAAATGATCCCCGGCGgAGtGTCcCGcAAAttTGGGTAAGGTC

SEQ ID NO: ISOLATE

145	DK13	367	ATCGATACcCTAACTTGGGScTTCGCCGAcCTCATGGGATACATCCCCgTCGTAGGCGCCCC
143	Z6	367	ATCGATACcCTAACTTGGGScTTCGCCGAcCTCATGGGATACATCCCCGTCGTAGGCGCCCC
144	Z7	367	ATCGATACcCTAAcTGGGScTTCGCCGAcCTCATGGGATACATCCCCGTCGTAGGCGCCCC
140	Z8	367	ATCGATACcCTAcGTGCGScTTCGCCGAcCTCATGGGATACATCCCCGTCGTAGGCGCCCC
139	Z4	367	ATCGATACcCTGACGTGCGScTTCGCCGAcCTCATGGGATACATCCCCgTCGTAGGCGCCCC
142	Z5	367	ATCGATACcCTGACGTGCGScTTCGCCGAcCTCATGGGATACATCCCCgTCGTAGGCGCCCC
141	Z1	367	ATCGATACcCTGACGTGCGScTTCGCCGAcCTCATGGGATACATCCCCGTCGTAGGCGCCCC

139-145 consensus ATCGATACcCT-ACgTGcGcGCTTcGCCGAcCTCATGGGATACATcCCGcTCGTAGGCGCCCC

SEQ ID NO: ISOLATE

145	DK13	428	CCGTGGGTGGCGTCGCCAGAGCCCTGGCGCATGGcGTcAGGctTcTGGAGGACGGGgTCAA
143	Z6	428	CCGTGGGTGGCGTCGCCAGGGCCCTGGCaCATGGcGTTAGGGCTgTGGAGGACGGGATCAA
144	Z7	428	CCGTGGGTGGCGTCGCCAGGGCCCTaGCGCATGGCGTTAGGGCTcTGGAGGACGGGATCAA
140	Z8	428	CaGTaGgAGGGCTGCCAGAGCCCTGGCGCATGGCGTCAGGGCTGTGGAGGACGGGATCAA
139	Z4	428	CcGTgGgGGCGTCGCCAGGGcTcTGGCGCATGGCGTCAGGGCTGTGGAGGACGGGATCAA
142	Z5	428	CaGTaGgTGGCGTCGCCAGGGCCcTGGCGCATGGCGTCAGGGCCcTGGAGGACGGAAcCAA
141	Z1	428	CtGTgGgTGGCGTCGCCAGGGCCcTGGCGCATGGCGTCAGGGCCcTGGAGGACGGAAcCAA

139-145 consensus CcGTgGgTGGCGTCGCCAGGcGcCcTgGcGcCATGGcGTcAGGgctgTGGAGGACGGgATcAA

SEQ ID NO: ISOLATE

145	DK13	489	TTATGCAACAGGGAATCTTCCCGGTGTCTCTTCTCTATCTTCTCTTGGCACTTcTCG
143	Z6	489	TTATGCAACAGGGAATCTTCCCGGTGTCTCTTCTCTATCTTCTCTTGGCACTTCTTTCG
144	Z7	489	TTATGCAACAGGGAACCTTCCCGGTGTCTCTTCTCTATCTTCTCTTGGCACTTCTTTCG
140	Z8	489	CTATGCAACAGGGAACCTTCTCGGTGTCTCTTCTCTATCTTCTCTTGGCACTTCTcTCG
139	Z4	489	CTATGCAACAGGGAATCTTCCCGGTGTCTCTTCTCTATCTTCTCTTGGCACTTCTcTCG
142	Z5	489	CTATGCAACAGGGAATCTTCTCGGTGTCTCTTCTCTATCTTCTCTAaCTTGCACTTcTCTCG
141	Z1	489	CTAcGCAACAGGGAACCTTCTCGGTGTCTCTTCTCTATCTTCTCTcCTTGCACTTcTCTCG

139-145 consensus cTATgCAACAGGGAATCTTCCcGGTGTCTcTtTcTCTATCTTcTCTcTgGCACtTcTcTCG

SEQ ID NO: ISOLATE

145	DK13	550	TGCCTgACTGTTCcCGcTcTCGGCC
143	Z6	550	TGCCTaACTGTTCcCaACCTcCGGCC
144	Z7	550	TGCCTgACTGTTCcCGcCTcCGGCC
140	Z8	550	TGCCTaAcGTCcCAGCGTcTcGCT
139	Z4	550	TGCCTcAcTGTcCCAGCGTcGcCT
142	Z5	550	TGCtTGACAACACcGcCATTCcGCT
141	Z1	550	TGCcTGACAACACcAGCATTCcGcC

139-145 consensus TGCCTgACTgttCC-gC-TcGcCc

FIGURE 61

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG
1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG
1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG
1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG
1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG
1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG
1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG
1 ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG

ATGAGCACGAATCTAAACCTCAAAGAAAAACCAAGAAACACCAACCGCGCCACAGG

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG
62 ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG

ACGTCAAGTTCCCGGGCGGTGGTCAGATCGTTGGTGGAGTTACTTGTGTGCGCGCAGGGG

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGaCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGgCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGgCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGgCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCgGAACGGTCGCAACCCCGTGGgCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGaCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGaCGG
123 CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCAGAACGGTCGCAACCCCGTGGaCGG

CCCTAGgtTGGGTGTGCGCGGACTCGGAAGACTTCaGAACGGTCGCAACCCCGTGGgCGG

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

184 CGTCAGCCTATTCCCAAGGCGCGCAACcCaCGGGcCGGTCTCGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAACcCcCGGGcCGGTCTCGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAACcCACGGGcCGGTCTCGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAACcCACGGGcCGGTCTCGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAACcCACGGGcCGGTCTCGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAACcCACGGGcCGGTCTCGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAACcCACGGGcCGGTCTCGGGGTCAACCCGGGTACC
184 CGTCAGCCTATTCCCAAGGCGCGCAACcCACGGGcCGGTCTCGGGGTCAACCCGGGTACC

CGTCAGCCTATTCCCAAGGCGCGCAACcCaCGGGcCGGTCTCGGGGTCAACCCGGGTACC

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG
245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG
245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG
245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG
245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG
245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG
245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG
245 CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG

CTTGGCCCTTTTACGCCAATGAGGGCCTCGGGTGGGcAGGGTGGtTGCTCTCCCCCGAGG

FIGURE 61

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

SEQ ID NO: ISOLATE

153 SA11
152 SA6
146 SA4
147 SA5
148 SA7
149 SA1
150 SA3
151 SA13

146-153 consensus

306 CTCTCGGCTAAcTGGGGCCCCAATGACCCCCGGCGAAAgATCGCGCAATTGGGGcAAGGTC
306 CTCTCGGCTAAATTGGGGCCCCAATGACCCCCGGCGAAAAATCGCGCAATTGGGGTAAGGTC
306 CTCTCGGCTAAATTGGGGCCCCAATGACCCCCGGCGAAAgATCGCGCAATTGGGGTAAGGTC
306 CTCTCGGCTAAATTGGGGCCCCAATGACCCCCGGCGAAAgATCGCGCAATTGGGGTAAGGTC
306 CTCTCGGCTAAATTGGGGCCCCAATGACCCCCGGCGAAAgATCGCGCAATTGGGGTAAGGTC
306 CTCTCGGCTAAATTGGGGCCCCAATGACCCCCGGCGAAAgATCGCGCAATTGGGGTAAGGTC
306 CTCTCGGCTAAATTGGGGCCCCAATGACCCCCGGCGAAAgATCGCGCAATTGGGGTAAGGTC
306 CTCTCGGCTAAATTGGGGCCCCAATGACCCCCGGCGAAAgATCGCGCAATTGGGGTAAGGTC

CTCTCGGCTAAcTGGGGCCCCAATGACCCCCGGCGAAaATCGCGCAATTTGGGTAAGGTC

367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC
367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC
367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC
367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC
367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC
367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC
367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC
367 ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC

ATCGATACCCCTAACGTGCGGATTGCGCGACCTCATGGGGTACATCCCGCTCGTAGGCGGGCC

428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACACGGTGTGAGAGcCTTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACACGGTGTGAGGGTCTTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACATGGTGTGAGGGTCTTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACATGGTGTGAGGGTCTTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACACGGTGTGAGGGTCTTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACACGGTGTGAGGGTCTTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACACGGTGTGAGGGTCTTTGAGGACGGGGTAAA
428 CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACACGGTGTGAGGGTCTTTGAGGACGGGGTAAA

CCGTTGGGGGCGTCGCAAGGGCCTCTCGCACACGGTGTGAGGgTCTTTGAGGACGGGGTAAA

489 tTATGCAACAGGGAATtTCCCGGTGTGCTTTTCTCtATCTTTATCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCTATCTTTTgTCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCTATCTTTATCCTTGCACTTCTCTCG
489 CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCTATCTTTATCCTTGCACTTCTCTCG

CTATGCAACAGGGAATTTGCCCGGTGTGCTTTTCTCtATCTTTATCCTTGCACTTCTCTCG

550 TGCTgTgACCGTCCCGGcCaCTGCA
550 TGCTtAACCGTCCCTGCCTCTGCA
550 TGCTGACCGTCCCGGCTCTGCA
550 TGCTGACCGTCCCGGCTCTGCA
550 TGCTGACCGTCCCGGCTCTGCA
550 TGCTGACCGTCCCGGCTCTGCA
550 TGCTGACCGTCCCGGCTCTGCA
550 TGCTGACCGTCCCGGCTCTGCA
550 TGCTGACCGTCCCGGCTCTGCA

TGCTgTgACCGTCCCGGCTCTGcCa

FIGURE 6J

SEO ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

1 ATGAGCAGcaatCCTAAACCTCAAAGAAaAACcaAcGTAAcACcaACCGcCGCCACagG
1 ATGAGCACgAaTCTTAACCTCAAAGAAaAACCAACGTAACACCAaCCGcCGCCACAGG
1 ATGAGCACAAATCCCAAACTCAAAGAAaAACCAAGAAACCAACCGcCGCCACAGG
1 ATGAGCACATCTCTAAACCTCAAAGAAaAACCAAGAAACCAACCGTCTCGCCACAGG
1 ATGAGCACgAATCTTAACCTCAAAGAAaAACCAACGTAACACCAACCGcCGCCACAGG
1 ATGAGCACGAATCTTAACCTCAAAGAAaAACCAAGAAACCAACCGcCGCCACAGG
1 ATGAGCACACTCTCAAAACCCCAAAGAAaAACCAAGAAACCAACCGTCTCGCCACAGG

SEO ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

62 AegTcAAgTTcCCgGGcGGTGGTcCAGATCGTcGGTGGAGTtTAcTGTcTGCCGCGCAGGGG
62 ACGTcAAGTTCCCGGGcGGTGGTcCAGATCGTcGGTGGAGTtTAcTGTcTGCCGCGCAGGGG
62 ACGTcAAGTTcCCGGGcGGcGGcCAGATCGTcGGCGGAGTtTACTGTcTGCCGCGCAGGGG
62 ACGTcAAGTTCCCGGGTGGCGGACAGATCGTcGGTGGAGTtTAcTGTcTGCCGCGCAGGGG
62 ACGTAAaGTTCCCGGGTGGTGGcCAGATCGTcGGCGGAGTtTACTGTcTGCCGCGCAGGGG
62 AcGtAAGTTCCCGGGCGGTGGTcCAGATCGTcGGTGGAGTtTACTGTcTGCCGCGCAGGGG
62 ACGTCAAGTTCCCGGGTGGCGGTcCAGATCGTcGGCGGAGTtTACTGTcTGCCGCGCAGGGG

SEO ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

123 CCCcaGgtTGGGTGTGCGGcGgaCtaGgAagaCTTcGAgCGgTcGCAaCCtCgTGaaGg
123 CCCcaGgtTGGGTGTGCGGcGgaCtaGgAAGACTTcGAGCGgTcGCAACCTCGtGGaaGg
123 CCCcAGgtTGGGTGTGCGGcGCAcAAGGAgaCTTcGAgCGaTCCcAGCGcCGTGGgAGg
123 CCCcAGATtGGGTGTGCGGcGCGAGCGGTAAaACTTCTGAGCGGTcCaCAGCTCGCGAGCA
123 CCCcAGgtTGGGTGTGCGGcGgaCtGgAAGACTTcGAGCGGTcGCAACCTCGtGGcAGg
123 CCCtAggtTGGGTGTGCGGcGgaCTCGGAAGACTTcGaAACCGGTcCaACCCCGTGGgCGG
123 CCCCcGgtTGGGTGTGCGGcGCGAGGAAGACTTCCGAGCGATCCcAGCCcAGAGGcAGG

SEO ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

184 CGaCAGCCTATcCCaAgGctCGcGggccgagGgCaggtcCTGGGctcagCCcGGtAcC
184 CGaCAaCCTATCCCCAAGGCTCGcGggCCCGAGGGcAGGgCCTGGGCTcAGCCcGGTAcC
184 CGCCAGCCCATCCCGAAGATCGGCGcCCAcTGGCAAGtCCTGGGGAaCaCAGGATATC
184 CGACAGCCTATCCCCAAGGCGCGTGGAGCGGAAGGCCGgTCTGGGCTCAGCCcGGGTACC
184 CGtCAGCCTATCCCCAAGGCaCGTcGggtcCGAGGGcAGTCTCTGGGCTcAGCCcGGGTAcC
184 CGcCAGCCTATCCCCAAGGCGcCGCAaCCcCGGcCGGTCTCTGGGCTcCAACCCGGGTACC
184 CGCCAACTATACCAAGGCGCGCCAGCCCGCAGGGcAGGCACTGGGCTCAGCCCGGATACC

SEO ID NO: Genotype
103-154 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

245 CtTGGCCcctTatGgaAatGAgGGctcGggTGGGCaGGAATGGcTccTgTcCCcCgcGG
245 CtTGGCCCTCTAtGgCaAtGAGGGcttgGgTGGGCaGGATGGCTCTGTCTCaCCCCgtGG
245 CtTGGCCcTgTAtGgAAtGAGGGcctCGGcTGGGCaGgtTGGCTCTGTCTCCCCCGcGG
245 CTGGCCCTCTAtGgAAtGAGGGcTGGGCGGCGGAGGcTGGCTCTGTCTCCCCCGcGG
245 CtTGGCCCTCTAtGgAAtGAGGGcTGGGCGGCGGAGGcTGGCTCTGTCTCCCCCGcGG
245 CTGGCCCTCTAtGgAAtGAGGGcTGGGCGGCGGAGGcTGGCTCTGTCTCCCCCGcGG
245 CTGGCCCTCTTATGGAaACGAGGGcTGGGCGGCGGAGGcTGGCTCTGTCTCCCCCGcGG

SEO ID NO: Genotype
103-153 cons.

103-124 1
125-134 2
135-138 3
139-145 4
146-153 5
154 6

306 cTctcggCctagtTGGGGcCccActGAcCCCGGcGtaggTcGCGCAaTtTGGGtAagGTC
306 cTctCGGCTAtTGGGGCCcCaGACCCCGGcGtaggTcGCGCAaTtTGGGtAagGTC
306 cTctCGcCctctTGGGGCCCAcActGAcCCCGGcGtaggTcGCGCAaTtTGGGtAagGTC
306 CTCCCGCTCATCTTGGGGCCCAcActGACCCCGGcGtaggTcGCGCAaTtTGGGtAagGTC
306 cTctCGGcGgTCTTGGGGcCcaAATGATCCCGGCGgagGtCcCGCAaTtTGGGtAagGTC
306 CTCTCGGCTAaTtTGGGGCCCAcActGACCCCGGcGtaggTcGCGCAaTtTGGGtAagGTC
306 CTCCCGGCCCATtTGGGGCCCAcActGACCCCGGcGtaggTcGCGCAaTtTGGGtAagGTC

FIGURE 6J

<u>SEQ ID NO:</u>	<u>Genotype</u>		
103-154	cons.	367	ATCGATACccTcACgTGcgGctTcGCCGAcCTCATGGGgTACaTcCCgcTCGTcGGcGccc
103-124	1	367	ATCGATACCCCTcAcATGCGGGTTCGCCGACCTCATGGGGTACATtCCGCTCGTCGGcGccc
125-134	2	367	ATCGATACCCcTaACgTGcgGctTTGCCGACCTCATGGGgTACaTcCCcGTCGTtLGGCGccc
135-138	3	367	ATCGATACCCCTtACGTGCGGgATTGCCGACCTCATGGGGTACATCCCGCTCGTCGGCGGCTC
139-145	4	367	ATCGATACcCTgACgTGcGGcTTcGCCGAcCTCATGGGATACATcCCGcTCGTaAGCGCCCC
146-153	5	367	ATCGATACCCTaACgTGCGGgATTGCCGAcCTCATGGGGTACATCCCGCTCGTAGGCGGCC
154	6	367	ATCGATACCCTaACGTGTGGGTTCGCCGATCTCATGGGGTACATtCCCGCTCGTGGGCGGCC
<u>SEQ ID NO:</u>	<u>Genotype</u>		
103-154	cons.	428	CcgTaGGgGGcGtcGCGaggGCCcTgGCGCaTGGcGTcaGggttcTgGAGACGGggTgAA
103-124	1	428	CccTaGGgGGcGcTGCCAGgGcCTGGCGCaTGGcGTCCGgGtcTGGAGGACGGCGTGAA
125-134	2	428	CggTtGGaGGcGtcGCCAGGCTCTgGCaCaTGGtGTgAGgGtcCTGGAGGACGGgATaAA
135-138	3	428	CcGTAGGaGGcCTCGCAAGGCCCTCGCGCATGGCGCTGAGGGCCCTTGAAGACGGGATaAA
139-145	4	428	CcGTgGctGGCTCGCGAGgGcCTgGCGCaTGGcCTcAGggtgTGGAGGACGGgATcAA
146-153	5	428	CCGTGGGGCGCTCGCAAGGGctCTcGCAcAcGGTGTGAGgGctCTTGAGGACGGGGTAA
154	6	428	CTTTGGCGGGCTCGCGGCTGCGCTCGCACATGGCGTGAGGGCAATCGAGGACGGGATCA
<u>SEQ ID NO:</u>	<u>Genotype</u>		
103-154	cons.	489	cTatGCAACaGGgAAAtTgCCcGGTGTCTcTTCTCTATcTTcTcTcTgGctcTgcTgTcc
103-124	1	489	cTatGCAACAGGGAAAtTgCCcGGTGTCTcTTCTCTATcTTCTCTcTgGcttTgcTgTcc
125-134	2	489	tTAtGCAACaGGgAAAtTgCctGGTGTCTcTTtCTCTATcTTctTgcTtGcCctTcTGTcc
135-138	3	489	TTTtGCAACAGGGAACTTGCCGGTGTCTcTTTCTCTATcTTCTCTTgGctcTgTtTCTcT
139-145	4	489	cTAtGCAACAGGGAAAtCTTCCcGGTGTCTcTTCTCTATcTTcTctTgGCACtTcTcTCG
146-153	5	489	cTAtGCAACaGGGAAtTgCCCGGTGTCTcTTTCTCTATcTTTaTCTTGCACtTCTcTCg
154	6	489	TTATGCAACAGGGAAATCTCCCGGTGTCTcTTTCTCTATcTTCTTTTGGCACTACTCTCG
<u>SEQ ID NO:</u>	<u>Genotype</u>		
103-154	cons.	550	TGcctgaccgtcCCAgcttCtgcT
103-124	1	550	TGttTgACcatcCCaGctTcGcT
125-134	2	550	TGcatCaCagtgCCaGtgTcTgCt
135-138	3	550	TGctTAaTTCATCCaGcAGCTAGT
139-145	4	550	TGcGTgACtggtCCagCgTgGcC
146-153	5	550	TGccTgAccgTCCGgGCTcTgCa
154	6	550	TGCGTCACAACCCAGCTTCGGCT

FIGURE 7A

SEQ ID NO: ISOLATE

156 US11
157 S14
158 SW1
159 S18
160 DR4
155 DK7

155-160 consensus

1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

SEQ ID NO: ISOLATE

156 US11
157 S14
158 SW1
159 S18
160 DR4
155 DK7

155-160 consensus

62 RQIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLKGV
62 RQIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLKGV
62 RQIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLKGV
62 RQIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLKGV
62 RQIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLKGV
62 RQIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLKGV

RQIPKARRPEGRRTWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPTDPRRRSRNLKGV

SEQ ID NO: ISOLATE

156 US11
157 S14
158 SW1
159 S18
160 DR4
155 DK7

155-160 consensus

123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

IDTLTCGFADLMGYIPLVGAPLGGAARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS

SEQ ID NO: ISOLATE

156 US11
157 S14
158 SW1
159 S18
160 DR4
155 DK7

155-160 consensus

184 CLTVPASA
184 CLTVPASA
184 CLTVPASA
184 CLTVPASA
184 CLTVPASA
184 CLTVPASA

CLTVPASA

FIGURE 7B

SEQ ID NO:	ISOLATE	
175	P8	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
170	IND8	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
162	S45	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
171	S9	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
163	D1	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
165	P10	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
169	IND3	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
164	US6	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
166	DK1	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
167	T10	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
168	SW2	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
161	SA10	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
174	HK4	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
172	HK3	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
176	T3	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
173	HK5	1 MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

161-176 consensus MSTNPKPQRKTKRNTNRPPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

SEQ ID NO:	ISOLATE	
175	P8	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
170	IND8	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
162	S45	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
171	S9	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
163	D1	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
165	P10	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
169	IND3	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
164	US6	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
166	DK1	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
167	T10	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
168	SW2	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
161	SA10	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
174	HK4	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
172	HK3	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
176	T3	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV
173	HK5	62 RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV

161-176 consensus RQPIPKARRPEGRAWAQPGHPWPLYANEGLGWAGWLLSPRGSRPSWGPTDPRRRSRLNLGV

SEQ ID NO:	ISOLATE	
175	P8	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
170	IND8	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
162	S45	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
171	S9	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
163	D1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
165	P10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
169	IND3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
164	US6	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
166	DK1	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
167	T10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
168	SW2	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
161	SA10	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
174	HK4	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
172	HK3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
176	T3	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS
173	HK5	123 IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS

161-176 consensus IDTLTCGFADLMGYIPLVGAPLGGVARALAHGVRVLEDGVNATGNLPGCSFSIFLLALLS

SEQ ID NO:	ISOLATE
175	P8
170	IND8
162	S45

184 CLTiPASA
184 CLTiPASA
184 CLTiPASA

FIGURE 7B

171	S9	184	CLTiPASA
163	D1	184	CLTiPASA
165	P10	184	CLTiPASA
169	IND3	184	CLTiPASA
164	US6	184	CLTiPASA
166	DK1	184	CLTiPASA
167	T10	184	CLTiPASA
168	SW2	184	CLTiPASA
161	SA10	184	CLTiPASA
174	HK4	184	CLTiPASA
172	HK3	184	CLTiPASA
176	T3	184	CLTiPASA
173	HK5	184	CLTiPvSA
161-176	consensus		CLTiPaSA

2025

155-176 consensus IDTLTCGFADLMGYIPLVGaPLGGaARALAHGVRVLEDGVNYATGNIPGCsFSIELLALLS

[illegible]

FIGURE 7D

SEQ ID NO:	ISOLATE	
179	T9	1 MSTNPKPQRKtIRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
178	US10	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
180	T2	1 MSTiPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177	T4	1 MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
177-180	consensus	MSTnPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
179	T9	62 RQPIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPdPRHRSRNVGKV
178	US10	62 RQPIPKDRRpTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPtDPRHRSRNVGKV
180	T2	62 RQPIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177	T4	62 RQPIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPNDPRHRSRNVGKV
177-180	consensus	RQPIPKDRRsTGKSWGKPGYPWPPLYGNEGLGWAGWLLSPRGSRPSWGPnDPRHRSRNVGKV
SEQ ID NO:	ISOLATE	
179	T9	123 IDTLTCGFADLMGYiPVVGaPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
178	US10	123 IDTLTCGFADLMGYiPVVGaPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
180	T2	123 IDTLTCGFADLMGYiPVVGaPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
177	T4	123 IDTLTCGfADLMGYvPVVGgPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
177-180	consensus	IDTLTCGfADLMGYiPVVGaPLGGVARALAHGVRVLEDGVNYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
179	T9	184 CITtPaSA
178	US10	184 CITiPVSA
180	T2	184 CITiPVSA
177	T4	184 CITiPVSA
177-180	consensus	CITiPvSA

FIGURE 7E

SEQ ID NO:	ISOLATE	
183	DK11	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
184	SW3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
181	T8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
182	US1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
185	DK8	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKsERSQPRGR
181-185	consensus	MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRaTRKtSERSQPRGR
SEQ ID NO:	ISOLATE	
183	DK11	62 RQIPKDRRSTGKpWGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV
184	SW3	62 RQIPKDRRSTGKSwGKPGYPWPLYGNEGCGWAGWLLSPRGSHPNWGPTDPRHRSRNLGKV
181	T8	62 RQIPKDRRSTGKSwGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGv
182	US1	62 RQIPKDRRSTGKSwGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
185	DK8	62 RQIPKDRRSTGKSwGKPGYPWPLYGNEGCGWAGWLLSPRGSRPTWGPTDPRHRSRNLGKV
181-185	consensus	RQIPKDRRSTGKsWGKPGYPWPLYGNEGCGWAGWLLSPRGsRptWGPTDPRHrSRNLGkv
SEQ ID NO:	ISOLATE	
183	DK11	123 IDTITCGFADLMGYI PVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
184	SW3	123 IDTITCGFADLMGYI PVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
181	T8	123 IDTITCGFADLMGYI PVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
182	US1	123 IDTITCGFADLMGYI PVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
185	DK8	123 IDTITCGFADLMGYI PVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
181-185	consensus	IDTITCGFADLMGYI PVVGAPVGGVARALAHGVRVLEDGINYATGNLPGCSFSIFLLALLS
SEQ ID NO:	ISOLATE	
183	DK11	184 CcTVPVSA
184	SW3	184 CFTVPVSA
181	T8	184 CFTVPVSA
182	US1	184 CaTVPVSA
185	DK8	184 CcTVPVSA
181-185	consensus	C-TVPVSA

FIGURE 7F

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

SEQ ID NO: ISOLATE

183 DK11
184 SW3
181 T8
182 US1
185 DK8
186 S83
178 US10
180 T2
179 T9
177 T4

177-186 consensus

1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRtTRKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR
1 MSTNPKPQRTKRNTNRRPQDVKPGGGQIVGGVYLLPRRGPRLGVRATrKTSERSQPRGR

MSTnPKPQRTkRnTnRRPQDVkPGGGQIVGGVYLLPRRGPRLGVRaTrKtTSERSQPRGR

62 RQPIPKDRRSTGKpWGKPGYPWFLYNGEGCGWAGWLLSPRGSHPNWGPtDPRHkSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSHPNWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV
62 RQPIPKDRRSTGKsWGKPGYPWFLYNGEGCGWAGWLLSPRGSRPTWGPtDPRHRSRNLGKV

RQPIPKDRRSTGKsWGKPGYPWFLYNGEG-GWAGWLLSPRGSRPswGPTDPRHrSRNLGKV

123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTITCGFADLMGYiPVVGAPVGGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTLTCGFADLMGYiPVVGAPLGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTLTCsLADLMGYiPVVGAPLGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS
123 IDTLTCsLADLMGYiPVVGAPLGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS

IDT-TCGfADLMGYiPVVGAPvGGVARALAHGVRVLEDGINyATGNLPGCSFSiFLLALLS

184 CctVPVSA
184 CFTVPVSA
184 CFTVPVSA
184 CatVPVSA
184 CctVPVSA
184 CIsVPVSA
184 CItIPVSA
184 CItIPVSA
184 CItIPaSA
184 CItIPvSA

CItvPvSA

FIGURE 7G

SEQ ID NO:	ISOLATE	
189	S2	1 MSTLKPQRTKRNITRRPDvKFPGGGQIVGGVYVLPRRGPRLGVRATRTKTSERSQPRGR
187	HK10	1 MSTLKPQRTKRNITRRPDVVKFPGGGQIVGGVYVLPRRGPRLGVRATRTKTSERSQPRGR
190	DK12	1 MSTLKPQRTKRNITRRPDVVKFPGGGQIVGGVYVLPRRGPRLGVRATRTKTSERSQPRGR
188	S52	1 MSTLKPQRTKRNITRRPDVVKFPGGGQIVGGVYVLPRRGPRLGVRATRTKTSERSQPRGR
187-190	consensus	MSTLKPQRTKRNITRRPDvKFPGGGQIVGGVYVLPRRGPRLGVRATRTKTSERSQPRGR
SEQ ID NO:	ISOLATE	
189	S2	62 RQPIPKARRSEGRSWAQPGYPWFLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187	HK10	62 RQPIPKARRSEGRSWAQPGYPWFLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
190	DK12	62 RQPIPKARRSEGRSWAQPGYPWFLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
188	S52	62 RQPIPKARRSEGRSWAQPGYPWFLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
187-190	consensus	RQPIPKARRSEGRSWAQPGYPWFLYGNEGCGWAGWLLSPRGSRPSWGPNDPRRRSRNLGKV
SEQ ID NO:	ISOLATE	
189	S2	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187	HK10	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
190	DK12	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
188	S52	123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
187-190	consensus	IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRALEDGINFATGNLPGCSFSIFLLALFS
SEQ ID NO:	ISOLATE	
189	S2	184 CLIHPAAS
187	HK10	184 CLIHPAAS
190	DK12	184 CLIHPAAS
188	S52	184 CLVHPAAS
187-190	consensus	CLIHPAAS

FIGURE 7H

SEO ID NO: ISOLATE

194 Z5
193 Z1
192 Z8
195 Z6
196 Z7
191 Z4
197 DK13

191-197 consensus

1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
1 MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

MSTNPKPQRKTKRNTNRRPMDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR

SEO ID NO: ISOLATE

194 Z5
193 Z1
192 Z8
195 Z6
196 Z7
191 Z4
197 DK13

191-197 consensus

62 RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV
62 RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV
62 RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV
62 RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV
62 RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV
62 RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV
62 RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV

RQIPiPARRSEGRSWAQPGYPWPLYGNEGCGWAGWLLSPRGRSPSWGPNDRRRSRNLGKV

SEO ID NO: ISOLATE

194 Z5
193 Z1
192 Z8
195 Z6
196 Z7
191 Z4
197 DK13

191-197 consensus

123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS
123 IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS

IDTLTCGFADLMGYIPLVGAPVGGVARALAHGVRAVEDGINYATGNLPGCSFSIFLLALLS

SEO ID NO: ISOLATE

194 Z5
193 Z1
192 Z8
195 Z6
196 Z7
191 Z4
197 DK13

191-197 consensus

184 CLITPASA
184 CLITPASA
184 CLITPASA
184 CLITPASA
184 CLITPASA
184 CLITPASA
184 CLITPASA

CLITvPaSA

194 Z5
193 Z1
192 Z8
195 Z6
196 Z7
191 Z4
197 DK13

FIGURE 71

SEQ ID NO:	ISOLATE	
205	SA11	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
202	SA3	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
198	SA4	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
199	SA5	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
200	SA7	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
203	SA13	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
201	SA1	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
204	SA6	1 MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
198-205	consensus	MSTNPKPQRKTKRNTNRRPQDVKFPGGGQIVGGVYLLPRRGPRLGVRATRKTSERSQPRGR
SEQ ID NO:	ISOLATE	
205	SA11	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
202	SA3	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
198	SA4	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
199	SA5	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
200	SA7	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
203	SA13	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
201	SA1	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
204	SA6	62 RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
198-205	consensus	RQIPKARQPTGRSWGQPGYPWPFLYANEGLGwAGWLLSPRGSRPnWGPNDRRKSRNLGKV
SEQ ID NO:	ISOLATE	
205	SA11	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
202	SA3	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
198	SA4	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
199	SA5	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
200	SA7	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
203	SA13	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
201	SA1	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
204	SA6	123 IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
198-205	consensus	IDTLTCGFADLMGYIPLVGGPVGGVARALAHGVRvLEDGVNYATGNLPGCSFSIFILALLS
SEQ ID NO:	ISOLATE	
205	SA11	184 CLTVPaSA
202	SA3	184 CLTVPaSA
198	SA4	184 CLTVPaSA
199	SA5	184 CLTVPaSA
200	SA7	184 CLTVPaSA
203	SA13	184 CLTVPaSA
201	SA1	184 CLTVPaSA
204	SA6	184 CLTVPaSA
198-205	consensus	CLTVPaSA

FIGURE 7J

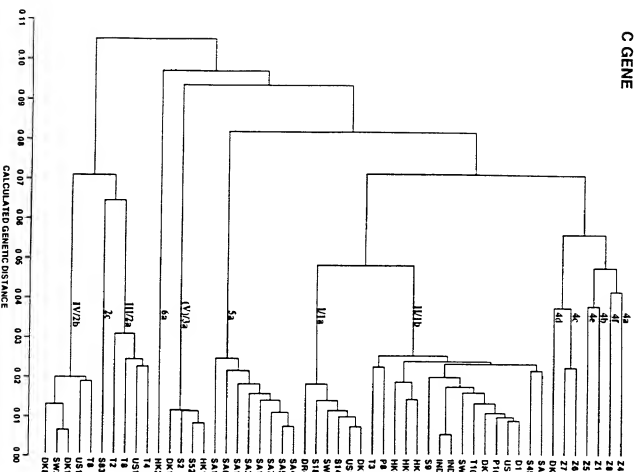
SEQ ID NO: 155-206	Genotype cons.	1	MSTAPKQPKTKRNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKLSERSQPRRRQDIPKARIPGRGSRMaqGgypmPlygnEGcgWAGW
155-176	type 1		MSTAPKQPKTKRNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKLSERSQPRRRQDIPKARIPGRGSRMaqGgypmPlygnEGcgWAGW
177-186	type 2		MSTAPKQPKTKRNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKLSERSQPRRRQDIPKARIPGRGSRMaqGgypmPlygnEGcgWAGW
187-190	type 3		MSTAPKQPKTKRNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKLSERSQPRRRQDIPKARIPGRGSRMaqGgypmPlygnEGcgWAGW
191-197	type 4		MSTAPKQPKTKRNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKLSERSQPRRRQDIPKARIPGRGSRMaqGgypmPlygnEGcgWAGW
198-205	type 5		MSTAPKQPKTKRNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKLSERSQPRRRQDIPKARIPGRGSRMaqGgypmPlygnEGcgWAGW
198-206	type 6		MSTAPKQPKTKRNTNRPPQDVKFGGGQIVGGVYLLPRRGPRLGVRATRKLSERSQPRRRQDIPKARIPGRGSRMaqGgypmPlygnEGcgWAGW
SEQ ID NO: 155-206	Genotype cons.	97	LLSPGSRPamGpTDPRTTSNIGKVDTITCGfADLMGYiPIVGaPIGGVaRALAHGVRVLEDGvNYATGNIPGCcFSIFILALISCLITvPasa
155-176	type 1		LLSPGSRPamGpTDPRTTSNIGKVDTITCGfADLMGYiPIVGaPIGGVaRALAHGVRVLEDGvNYATGNIPGCcFSIFILALISCLITvPasa
177-186	type 2		LLSPGSRPamGpTDPRTTSNIGKVDTITCGfADLMGYiPIVGaPIGGVaRALAHGVRVLEDGvNYATGNIPGCcFSIFILALISCLITvPasa
187-190	type 3		LLSPGSRPamGpTDPRTTSNIGKVDTITCGfADLMGYiPIVGaPIGGVaRALAHGVRVLEDGvNYATGNIPGCcFSIFILALISCLITvPasa
191-197	type 4		LLSPGSRPamGpTDPRTTSNIGKVDTITCGfADLMGYiPIVGaPIGGVaRALAHGVRVLEDGvNYATGNIPGCcFSIFILALISCLITvPasa
198-205	type 5		LLSPGSRPamGpTDPRTTSNIGKVDTITCGfADLMGYiPIVGaPIGGVaRALAHGVRVLEDGvNYATGNIPGCcFSIFILALISCLITvPasa
198-206	type 6		LLSPGSRPamGpTDPRTTSNIGKVDTITCGfADLMGYiPIVGaPIGGVaRALAHGVRVLEDGvNYATGNIPGCcFSIFILALISCLITvPasa

FIGURE 7E

SEQ ID NO:	Genotype	10	20	30	40	50	60	70	80	90
155-160	I/1a	MTSTPAPRNTNTNTPDQKTEPCGGG	VGQVTLIPREPRICVRATKTSERSQPGCRDPTIPAR	PGGSLGAPGPPVPIVPGEGGAGCU						
151-176	I/1b	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
151-176	I/1b	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
181-185	IV/2a	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
186	2c	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
187-190	(V)/3a	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
191	4a	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
191	4b	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
195	4c	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
197	4d	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
194	4e	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
196	5a	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
198-205	5b	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					
206	6a	M--K-K-MR-Q-V	L--L--A-T	K-A-P-E-R-T-AQ-Y	L-GM-CG					

SEQ ID NO:	Genotype	100	110	120	130	140	150	160	170	180	190
155-160	I/1a	LLSPFGSPANGDPRRNRNIGAVDITTCGADLNCITPI	VGAPIGGVALANGVRVIEDGVKATGMIPGCEFSIFILA	ISCI	TV	PSA					
161-180	I/1b	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
177-180	I/1/2a	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
181-185	IV/2a	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
186	2c	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
191-190	(V)/3a	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
191	4a	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
191	4b	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
193	4c	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
195	4d	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
197	4e	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
199	4f	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
192	5a	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
198-205	5b	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---
206	6a	---R-R-S-P1--RR--L-K--L--GF	---L-A-L-A-R-R--VL--V-Y--L--S--	---	---	---	---	---	---	---	---

C GENE



E1 GENE

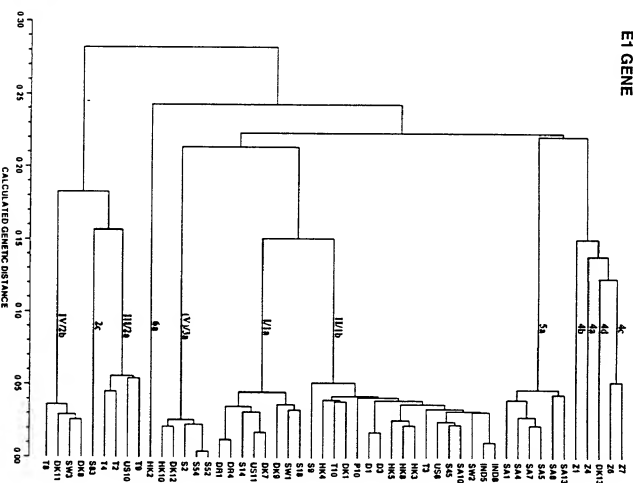


FIGURE 8

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) : Jens Bukh, et al

Serial No. : 08/290,665

Group Art Unit: To be assigned

Filed : August 15, 1994

Examiner: To be assigned

For : NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE E
ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS
AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN
DIAGNOSTIC METHODS AND VACCINES

Hon. Commissioner of Patents and Trademarks
Washington, D.C. 20231

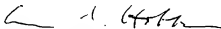
ASSOCIATE POWER OF ATTORNEY

Dear Sir:

Pursuant to the provisions of 37 CFR 1.33 and 1.34 and MPEP 402.02, the undersigned attorney of record hereby appoints the following as associate attorneys to prosecute this application, to receive the patent, and to transact all business in the Patent and Trademark Office in connection with the above-identified application:

Kurt E. Richter (Reg. No. 24,052); Eugene Moroz (Reg. No. 25,237); William S. Feiler (Reg. No. 26,728); Israel Blum (Reg. No. 26,710); Bartholomew Verdirmo (Reg. No. 28,483); Maria C. H. Lin (Reg. No. 29,323); Christopher E. Chalsen (Reg. No. 30,936); Eugene C. Rzucidlo (Reg. No. 31,900); Mary J. Morry (Reg. No. 34,398); Michael M. Murray (Reg. No. 32, 537); Jean E. Shimotake (Reg. No. 36,273); Kathryn M. Brown (Reg. No. 34,556); Leslie A. Serunian (Reg. No. 35,353); Dorothy R. Auth (Reg. No. 36,434); Richard W. Bork (Reg. No. 36,459); M. Caragh Noone (Reg. No. 37,197); David V. Rossi (Reg. No. 36,659) and Carol M. Gruppi (Reg. No. 37,341) of Morgan & Finnegan whose address is: 345 Park Avenue, New York, New York 10154.

Respectfully submitted,

Date 12/15/94
Ann S. Hobbs
Registration No. 36,830

Patent Branch
Office of Technology Transfer
National Institutes of Health
Box 13
6011 Executive Boulevard, Suite 325
Rockville, MD 20852
Tel. No. (301) 496-7056

COMBINED DECLARATION AND POWER OF ATTORNEY

As a below named inventor, I hereby declare that my residence, post office address and citizenship are as stated below next to my name, the information given herein is true, that I believe I am the original, first and sole (if only one name is listed below) or an or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled: NUCLEOTIDE AND DEDUCED AMINO ACID SEQUENCES OF THE ENVELOPE 1 AND CORE GENES OF ISOLATES OF HEPATITIS C VIRUS AND THE USE OF REAGENTS DERIVED FROM THESE SEQUENCES IN DIAGNOSTIC METHODS AND VACCINES

which is described in:

☐ the attached application or

☐ PCT International Application No. _____ filed _____

☒ the specification in application Serial No. 08/290,665 filed August 15, 1994

(if applicable) and amended on _____

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose all information known to me which is material to the examination of this application in accordance with Title 37, Code of Federal Regulations, §1.56 (a).

I hereby claim foreign priority benefits under Title 35 United States Code, § 119 of any foreign application(s) for patent or inventor's certificate or of any PCT international application(s) designating at least one country other than the United States of America listed below and have also identified below any foreign applications(s) for patent or inventor's certificate or any PCT international applications(s) designating at least one country other than the United States of America filed by me on the same subject matter having a filing date before that of the application(s) of which priority is claimed.

COUNTRY	APPLICATION	DATE OF FILING (day, month, year)	PRIORITY CLAIMED UNDER 35 USC § 119
			<input type="checkbox"/> Yes <input type="checkbox"/> No
			<input type="checkbox"/> Yes <input type="checkbox"/> No
			<input type="checkbox"/> Yes <input type="checkbox"/> No

I hereby claim the benefit under Title 35, United States Code §120 of any United States application(s) or PCT International application(s) designating the United States of America that is/are listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in that/those prior application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56(a) which occurred between the filing date of the prior application(s) and the national or PCT international filing date of this application.

Application Serial No.	Filing Date	Status: patented, pending, abandoned
08/086,428	29 June 1993	pending

I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

James C. Haight, Reg. No. 25,588; Gloria Richmond, Reg. No. 30,416; Robert Benson, Reg. No. 33,612; Jack Spiegel, Reg. No. 34,477; Laurence J. Hyman, Reg. No. 35,551; Denise C. Bernstein, Reg. No. 35,787; Susan S. Rucker, Reg. No. 35,762; David R. Sadowski, Reg. No. 32,808 and Ann S. Hobbs, Reg. No. 36,830 and Arthur J. Cohn, Reg. No. 37,800 all of the Office of Technology Transfer, National Institutes of Health, 6011 Executive Boulevard, Suite 325, Rockville, MD 20852

I further direct that all correspondence concerning this application be directed to:

Patent Branch
Office of Technology Transfer
National Institutes of Health
Box 13
6011 Executive Boulevard, Suite 325
Rockville, MD 20852
Telephone: (301) 496-7056

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Full Name of first joint inventor: Jens Bukh

Inventor's signature: *Jens Bukh* Date: 12/15/94

Country of Citizenship: Denmark

Residence: 5805 Sonoma Road, Bethesda, Maryland 20817, U.S.A.

Post Office Address: 5805 Sonoma Road, Bethesda, Maryland 20817, U.S.A.

Full Name of second joint inventor: Roger H. Miller

Inventor's signature: *Roger H. Miller* Date: 12/15/94

Country of Citizenship: United States of America

Residence: 15504 White Willow Lane, Rockville, Maryland 20853, U.S.A.

Post Office Address: 15504 White Willow Lane, Rockville, Maryland 20853, U.S.A.

Full Name of third joint inventor: Robert H. Purcell

Inventor's signature: *Robert H. Purcell* Date: 12/15/94

Country of Citizenship: United States of America

Residence: 17517 White Grounds Road, Boyds, Maryland 20841, U.S.A.

Post Office Address: 17517 White Grounds Road, Boyds, Maryland 20841, U.S.A.